

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 10, 2005, 21:23:50 ; Search time 329.5 Seconds
(without alignments)
5748.378 Million cell updates/sec

Title: US-10-054-683-18
Perfect score: 4796
Sequence: 1 catctgcacttccaactgc.....actgttaccatttcaaaaaa 2640

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2_1/USPRO pool_P/US10054683/runat_10012005_174509_15490/app_query.fasta_1.2823
-DB-A Geneseq_23Sep04 -OPMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US10054683 @CGN 1 1 398 @runat_10012005_174509_15490 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	3984	83.1	734	2	AAR87037
2	3984	83.1	734	6	ABJ19246 Human PH3
3	3984	83.1	734	7	ADB75186
4	3969.5	82.8	735	7	ADB75184 Prostate
5	3900	81.3	753	7	ADB75182 Prostate
6	3551	74.0	651	2	AAR87034 Human PH3
7	2440	50.9	735	2	AAR87036 Mouse PH3
8	1530	31.9	820	6	ABR39696 Human met
9	1524.5	31.8	787	5	AAU83636 Human PRO
10	1524.5	31.8	787	6	ABU80783 Human PRO

SUMMARIES

11	1524.5	31.8	787	6	ABO33749	Novel hum
12	1524.5	31.8	787	6	ABU82092	Novel hum
13	1524.5	31.8	787	6	ABJ72272	Human PRO
14	1524.5	31.8	787	6	ABJ72400	Human PRO
15	1524.5	31.8	787	6	ABO34295	Human sec
16	1524.5	31.8	787	7	ABJ72102	Human mem
17	1524.5	31.8	787	7	ADB83580	Novel hum
18	1524.5	31.8	787	7	ADB80686	Novel hum
19	1524.5	31.8	787	7	ADB73227	Novel hum
20	1524.5	31.8	787	7	ADB78309	Novel hum
21	1524.5	31.8	787	7	ADB84957	Human PRO
22	1524.5	31.8	787	7	ADB78063	Novel hum
23	1524.5	31.8	787	7	ADB87129	Human PRO
24	1524.5	31.8	787	7	ADB84711	Human PRO
25	1524.5	31.8	787	7	ADB83826	Novel hum
26	1524.5	31.8	787	7	ADB72981	Novel hum
27	1524.5	31.8	787	7	ADC36819	Human PRO
28	1524.5	31.8	787	7	ADC21809	Human PRO
29	1524.5	31.8	787	7	ADC49840	Novel hum
30	1524.5	31.8	787	7	ADC49039	Novel hum
31	1524.5	31.8	787	7	ADC49556	Novel hum
32	1524.5	31.8	787	7	ADC47417	Novel hum
33	1524.5	31.8	787	7	ADC47162	Novel hum
34	1524.5	31.8	787	7	ADC78037	Novel hum
35	1524.5	31.8	787	7	ADD06272	Novel hum
36	1524.5	31.8	787	7	ADC77791	Novel hum
37	1524.5	31.8	787	7	ADD50754	Novel hum
38	1524.5	31.8	787	7	ADD51000	Novel hum
39	1524.5	31.8	787	7	ADD50481	Human PRO
40	1524.5	31.8	787	7	ADD50235	Human PRO
41	1524.5	31.8	787	7	ADD51246	Novel hum
42	1524.5	31.8	787	8	ADC48793	Novel hum
43	1524.5	31.8	787	8	ADE20964	Novel hum
44	1524.5	31.8	787	8	ADE05808	Human PRO
45	1524.5	31.8	787	8	ADD75037	Human PRO

ALIGNMENTS

RESULT 1
AAR87037
ID AAR87037 standard; protein; 734 AA.
XX AAR87037;
AC AAR87037;
XX XX
DT 30-SEP-1996 (first entry)
XX XX
DE Human PH30 beta chain sperm protein.
XX XX
KW Human PH30 beta chain sperm protein; contraceptive;
KW FEE integrin binding domain.
XX XX
OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT Region 84..734
FT /note= "see AAR87035"
XX XX
PN WO9535118-A1.
XX XX
PD 28-DEC-1995.
XX XX
PF 06-JUN-1995; 95WO-US007295.
XX XX
PR 20-JUN-1994; 94US-00264101.
XX XX
PA (MERI) MERCK & CO INC.
XX XX
PI Alves K, Gupta SK, Hollis GF;
XX XX
DR WPI; 1996-058212/06.
DR N-PSDB; AAT07328.
XX XX

PT Human and mouse sperm protein PH30 beta chain and related DNA - useful in
 PT contraceptive vaccines.

XX Example 2; Page 45-48; 85pp; English.

XX Human PH30 beta chain sperm protein, having a FEE integrin binding
 CC domain, is 58.9% identical to mouse and 56.5% identical to guinea pig
 CC PH30 beta. The protein may be produced recombinantly and used in a
 CC contraceptive composition containing an effective adjuvant and an amount
 CC of sperm protein which is effective for the stimulation of antibodies
 CC which bind to sperm protein in vivo, thereby preventing or substantially
 CC reducing the rate of sperm-egg fusion

XX Sequence 734 AA;

Alignment Scores:

Pred. No.: 0 Length: 734
 Score: 3984.00 Matches: 734
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 83.07% Indels: 0
 DB: 2 Gaps: 0

US-10-054-683-18 (1-2640) x AAR87037 (1-734)

Qy 72 ATGTGGGTCTGTTCTCTCAGCGGCTCGCGGCTCGGATGAGCAGTAATTTTGTAT 131
 Db 1 MetTrpValLeuPheLeuLeuSerGlyLeuGlyLeuArgMetAspSerAsnPheAsp 20
 Qy 132 AGTTTACCTGTGCAAAATTTACAGTTCCGGAGAAATACGGTCAATTAATAAGGAAGAAATT 191
 Db 21 SerLeuProValGlnIleThrValProGluLysIleArgSerIleIleLysGluGlyLe 40
 Qy 192 GAATCGCAGGATCCTACAAATTTGTAATTCAGAGGAAACCATATCTGTAATTTAATG 251
 Db 41 GluSerGlnAlaSerTyLysIleValIleGluGlyLysProTyThrValAsnLeuMet 60
 Qy 252 CAAAAAATCTTTTACCCCATATTTAGAGTTTACAGTTTACGTGTCAGCAGGAAATTTATG 311
 Db 61 GlnLysAsnPheLeuProHisAsnPheArgValTySerTySerGlyThrGlyLeMet 80
 Qy 312 AAACCATCTGACCAAGATTTTTCAGAAATTTCCCACTACCAAGGGTATATTGAAGTTAT 371
 Db 81 LysProLeuAspGlnAspPheGlnAsnPheCysHisTyGlnGlyTyIleGluGlyTy 100
 Qy 372 CCAAAATCTGGTGATGGTTAGCACATGATGACTCGACTCAGGGCGTACTACAGTTTGA 431
 Db 101 ProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGlu 120
 Qy 432 AATGTTAGTTATGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAACATGTAATTTAC 491
 Db 121 AsnValSerTyGlyIleGluProLeuGluSerSerValGlyPheGluHisValIleTy 140
 Qy 492 CAAGTAAACATAGAAAGCAGATGTTTCCCTTATATATATAGAGAGGATTTGAATTAAGA 551
 Db 141 GlnValLysHisLysLysAlaAspValSerLeuTyAsnGluLysAspIleGluSerArg 160
 Qy 552 GATCTGCTTAAATTTACAAAGCGCAGCAGCCAGCAAGATTTTGCAGATATATAGAA 611
 Db 161 AspLeuSerPheLysLeuGlnSerAlaGluProGlnGlnAspPheAlaLysTyIleGlu 180
 Qy 612 ATGATGTTATAGTTGAAAAACAATTTGATATATCATATGCGGTCTGTATACAACTGTTGTC 671
 Db 181 MetHisValIleValGluLysGlnLeuTyAsnHisMetGlySerAspThrThrValVal 200
 Qy 672 GCTCAAAAGTTTCCAGTGTGATGAGTACGAAATGCTATTTTGTTCATTTAATATT 731
 Db 201 AlaGlnLysValPheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAsnIle 220
 Qy 732 ACAATTATCTCTTCTTCTGAGCTTTGGATAGATGAAATTAATAATTTGCAACCACTGGA 791
 Db 221 ThrIleIleLeuSerSerLeuGluLeuTrpIleAspGluAsnLysIleAlaThrThrGly 240

Qy 792 GAAGCTAATGAGTATTATACACATTTTAAAGATGGAATAAATCTTATCTTGTGTTACGT 851
 Db 241 GluAlaAsnGluLeuLeuHisThrPheLeuAGTTPLeuThrSerTyLeuValLeuArg 260
 Qy 852 CTTATGATGTGGCATTTTACTTTTACAGAGAAAGTCAATTTATCTTGTGTCGAACC 911
 Db 261 ProHisAspValAlaPheLeuLeuValTyArgGluLysSerAsnTyValGlyAlaThr 280
 Qy 912 TTTCAAGGGAAGATGTGTGATGCAAACTATGAGGAGGTGTGTCTCTGCACCCCAAGAAC 971
 Db 281 PheGlnGlyMetCysAspAlaMetTyAlaGlyValValLeuHisProArgThr 300
 Qy 972 ATAAGTCTGGAATCACTTCAGTATTATTTAGCTCAATATTAGAGCTTATGATGGGATC 1031
 Db 301 IleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyIle 320
 Qy 1032 ACTTATGATGACATTTAAACAATGCCAGTCTCAGGAGCTGTCTGCATTTATGATCCAGAA 1091
 Db 321 ThrTyAspAspIleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnProGlu 340
 Qy 1092 GCAATTCATTTCACTGCTGTGAAGATCTTTAGTAACCTGCAGCTTTCGAAGACTTTGCACAT 1151
 Db 341 AlaIleHisPheSerGlyValLysIlePheSerAsnCysSerPheGluAspPheAlaHis 360
 Qy 1152 TTTATTTCAAAGCAGAAAGTCCAGTCTCTTCAATCAGCTCGCTTAGATCTCTTTTTC 1211
 Db 361 PheIleSerLysGlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPhePhe 380
 Qy 1212 AAACACACAGCAGTGTGTGTAATGCAAGCTGGAAGCAGGAGAGAGTGTGCTGTGG 1271
 Db 381 LysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluGluCysAspCysGly 400
 Qy 1272 ACTGAACAGGATTTGTCCTTATTGGAGAAACATGTGTGATATTGCCCATGTAGATT 1331
 Db 401 ThrGluGlnAspCysAlaLeuIleGlyGluThrCysCysAspIleAlaThrCysArgPhe 420
 Qy 1332 AAAGCCGTTTCAACTGTGCTGAAGACCATGTCTGCGAAACACTGTCTATTATGTCAAA 1391
 Db 421 LysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSerLys 440
 Qy 1392 GAAGATGTGTAGGCTTCTTGAAGATGCGACTCCCTCAATATTGCAATGATCA 1451
 Db 441 GluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyCysAsnGlySer 460
 Qy 1452 TCTGCATCATGCCAGAAACCACTATGTTTCAGACTGGGCATCCGTGTGACTGAATCAA 1511
 Db 461 SerAlaSerCysProGluAsnHisTyValGlnThrGlyHisProCysGlyLeuAsnGln 480
 Qy 1512 TGGATCTGTATAGATGGAGTTTGTATGAGTGGGGATAAACAATGATACAGACATTTGGC 1571
 Db 481 TrpIleCysIleAspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPheGly 500
 Qy 1572 AAAGATGTAGGTTTGGCCCTTCAGATGTTATTCTCACCTTAATTTCAAGACTGATGTA 1631
 Db 501 LysGluValGluPheGlyProSerGluCysTySerHisLeuAsnSerLysThrAspVal 520
 Qy 1632 TCTGGAACCTGTGTATAGTGTATGAGTACACAGTGTGAAGTGTCAATCTGCAG 1691
 Db 521 SerGlyAsnCysGlyIleSerAspSerGlyTyThrGlnCysGluAlaAspAsnLeuGln 540
 Qy 1692 TGGGAAAAATTAATGTAATATGAGTAAATTTTATTTATTTATTTTATTTTCAAGGCCACT 1751
 Db 541 CysGlyLysLeuIleCysLysTyValGlyLysPheLeuLeuGlnIleProArgAlaThr 560
 Qy 1752 ATTATTTATGCCAACATAAGTGGACATCTCTGATTTCTCTGGAATTTGTCAGTGTATCAT 1811
 Db 561 IleIleTyAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAspHis 580
 Qy 1812 GCAGACACCAAGATGTGGAATAAAGATGGAATCTTCTTGTGTTCAATTAAGTTTGC 1871
 Db 581 AlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysValCys 600
 Qy 1872 AGGNATCAAGATGTGTGAGTTCTTCTACTACTTGGTTATGATTGTTACTACTGACAAATGC 1931

Db 601 ArgAsnGlnArgCysValSerSerSerTyrLeuGlyTyrAspCysThrThrAspLysCys 620
Qy 1932 AATGATAGAGTGATGCAATAACAAAAGCACTGTCTACCTGTAGTGTCTTCATATTTACCT 1991
Db 621 AsnAspArgGlyValCysAsnAsnLysHisCysHisCysSerAlaSerTyrLeuPro 640
Qy 1992 CCAGATTGCTCAGTTCAATCAGATCTATGCGCTGGAGTATGACAGTGGCAATTTT 2051
Db 641 ProAspCysSerValGlnSerAspLeuTrpProGlyGlySerLeuAspSerGlyAsnPhe 660
Qy 2052 CCACCTGTAGCTATACAGCCAGACTCCCTGAAGGCGCTACATTGAGAACATTTACCAT 2111
Db 661 ProProValAlaIleProAlaArgLeuProGluArgGlyIleGluAsnIleTyrHis 680
Qy 2112 TCCAAACCAATGAGATGCCATTTTCTTATTTCATCTCTTCTTCTTATTATTTCTGTGTA 2171
Db 681 SerLysProMetArgTrpProPhePheLeuPheIleProPhePheIlePheCysVal 700
Qy 2172 CTGATTGCTATAATGTGTGAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT 2231
Db 701 LeuIleAlaIleMetValLysValAsnPheGlnArgLysLysTrpArgThrGluAspTyr 720
Qy 2232 TCAGCGCATGCGCAACCTGAAAGTGAGAGTCAACCTAAAGG 2273
Db 721 SerSerAspGluGlnProGluSerGluSerGluProLysGly 734
RESULT 2
ABJ19246
ID ABJ19246 standard; protein; 734 AA.
XX AC ABJ19246;
XX DT 28-MAR-2003 (first entry)
XX DE Human cancer/testis antigen - SEQ ID NO 19.
XX KW Human; gene therapy; vaccine; cancer; cancer/testis antigen; CT antigen.
XX OS Homo sapiens.
XX PN WO200278526-A2.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-US009808.
XX PR 30-MAR-2001; 2001US-0280718P.
XX PR 20-APR-2001; 2001US-0285154P.
XX PR 05-OCT-2001; 2001US-0327432P.
XX PR 22-JAN-2002; 2002US-00054683.
XX (LUDW-) LUDWIG INST CANCER RES.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Old LJ, Scanlan MJ, Chen Y;
XX WPI; 2003-040608/03.
XX N-PSDB; ABT15727.
XX Diagnosing cancer comprises contacting a biological sample isolated from
PT a subject with an agent that specifically binds to a nucleic acid
PT molecule, its expression product or fragment or an antibody that binds to
PT the product or fragment.
XX Claim 36; Page 124-126; 155pp; English.
XX The invention comprises a method for diagnosing cancer, the method
XX involves detecting the DNA or protein sequences of human cancer/testis
XX (CT) antigens that are disclosed in the invention. The method of the
XX invention is useful for detecting/diagnosing, treating and monitoring a
XX cancer or condition characterised by the expression of a human CT
XX antigen. The present amino acid sequence represents a human CT antigen of

CC the invention
SQ Sequence 734 AA;
Alignment Scores:
Pred. No.: 0 3984.00 Length: 734
Score: 100.00% Matches: 734
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.07% Indels: 0
DB: 6 Gaps: 0
US-10-054-683-18 (1-2640) x ABJ19246 (1-734)
Qy 72 ATGTGGGTCTTGTTCCTCGCTCAGCGGCTCGCGGCTCGGATGGACAGTAATTTTGAT 131
Db 1 MetTrpValLeuPheLeuLeuSerGlyLeuGlyGlyLeuArgMetAspSerAsnPheAsp 20
Qy 132 AGTTTACCTGTGCNAATTACAGTTCGGAGAAAATACGTCATAATAAAGGAGGAATT 191
Db 21 SerLeuProValGlnIleThrValProGluLysIleArgSerIleIleLysGluGlyIle 40
Qy 192 GAATCGCAGGCATCTACAAAATTGTAATTTGAAGGGAACCATATATCTGTGAATTTAATG 251
Db 41 GluSerGlnAlaSerTyrLysIleValIleGluGlyLysProTyrThrValAsnLeuMet 60
Qy 252 CAAAAAACTTTTACCCCAATAATTTAGAGTTTACAGTTTATAGTGCACAGGAATATG 311
Db 61 GlnLysAsnPheLeuProHisAsnPheArgValTyrSerTyrSerGlyThrGlyIleMet 80
Qy 312 AAACCACTTGACCAAGATTTTTCAGAAATTTCTGCCACTTACCAGGGTATATGAAGTTAT 371
Db 81 LysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGlyTyr 100
Qy 372 CCAAAATCTGTGTGTAGTGTGTAGCACATGTACTGGACTCAGGGCGTACTACAGTTTGAA 431
Db 101 ProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGlu 120
Qy 432 AATGTTAGTTATGGAATPAGAACCCCTGGAGTCTTTCAGTCTGCTTTGAACATGTAATTTAC 491
Db 121 AsnValSerTyrGlyIleGluProLeuGluSerValGlyPheGluHisValIleTyr 140
Qy 492 CAAGTAAACATAAGAAAGCAGATGTTTCCTTATATATATAGAGAGGATATGAATCAAGA 551
Db 141 GlnValLysHisLysAlaAspValSerLeuTyrAsnGluLysAspIleGluSerArg 160
Qy 552 GATCTGTCTTTAAATTTACAAAGCGCAGAGCCAGCAAGATTTTGCAAAAGTATATAGAA 611
Db 161 AspLeuSerPheLysLeuGlnSerAlaGluProGlnGlnAspPheAlaLysTyrIleGlu 180
Qy 612 ATGCATGTTATAGTTGAAAAACAATTCATAATCATATGGGCTCTGATACAACTGTTGTC 671
Db 181 MetHisValIleValGluLysGlnLeuTyrAsnHisMetGlySerAspThrThrValVal 200
Qy 672 GCTCAAAAAGTTTTCAGTTGATTGGATTGAGCAATGCTATTTTGTTCATTAAATTT 731
Db 201 AlaGlnLysValPheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAsnIle 220
Qy 732 ACAATTTATCTGTCTTCATTTGGAGCTTTGGATAGATGAAATAAAATGCAACCACTGGA 791
Db 221 ThrIleIleLeuSerSerLeuGluLeuLeuTrpIleAspGluAsnLysIleAlaIleThrGly 240
Qy 792 GAAGCTAATGAGTTATTACACACATTTTTTAAGATGGAACACATCTTATCTTTGTTTACGT 851
Db 241 GluAlaAsnGluLeuLeuHisThrPheLeuArgTrpLysThrSerTyrLeuValLeuArg 260
Qy 852 CCTCATGATGTGGCATTTTACTTTGTTTACAGAAAAGTCAAAATTTATGTTGGTGCACACC 911
Db 261 ProHisAspValAlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAlaThr 280
Qy 912 TTTCAAGGGAAGATGTTGTGATGCAAACTATGCAGAGGTGTTGTTCTGCCACCCGACACC 971
Db 281 PheGlnGlyLysMetCysAspAlaAsnTyrAlaGlyGlyValValLeuHisProArgThr 300

Qy 972 ATAACTCTGGAATCACCTTGCAGTTATTTAGTCAATTAATTAGCCTTAGTATGGGATC 1031
Db |||||||
Qy 301 ILeSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyIle 320
Db |||||||
Qy 1032 ACTTATGATGACATTAAACAATGCCAGTCTCAGAGCTGTCTGCTGATTAATGAATCCAGAA 1091
Db |||||||
Qy 321 ThrTyrAspAspIleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnProGlu 340
Db |||||||
Qy 1092 GCAATTCATTTCACTGGTGTCAAGATCTTTAGTAACATGCAGCTTCGAGACTTGGACAT 1151
Db |||||||
Qy 341 AlaIleHisPheSerGlyValLysIlePheSerAsnCysSerPheGluAspPheAlaHis 360
Db |||||||
Qy 1152 TTTATTTCAACAGCAGAAGTCCAGTGTCTTACCAATCAGCTCGCTTGTAGATCTTTTTC 1211
Db |||||||
Qy 361 PheIleSerLysGlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPhePhe 380
Db |||||||
Qy 1212 AAACAGCAAGCAGTGTGTGTAATGCAAAAGCTGGAAGCAGAGAGGAGTGTGACTGTGGG 1271
Db |||||||
Qy 381 LysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluGluCysAspCysGly 400
Db |||||||
Qy 1272 ACTGAACAGGATGTGCCCTTATTGGAGAACATCTGTGTATTTGCCACATGTAGATT 1331
Db |||||||
Qy 401 ThrGluGlnAspCysAlaLeuIleGlyThrCysCysAspIleAlaThrCysArgPhe 420
Db |||||||
Qy 1332 AAAGCCGTTCAAACTGTCTGTAAGGACCATGCTGCGAAAACTGTCTATTATGTCAAAA 1391
Db |||||||
Qy 421 LysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSerLys 440
Db |||||||
Qy 1392 GAAAGATGTGTAGCTTCTTTGAAGAATGCGACCTCCTCGAATATTCGAATGGATCA 1451
Db |||||||
Qy 441 GluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGlySer 460
Db |||||||
Qy 1452 TCTGCATCATGCCAGAAAACCACTATGTTGAGTGGGATGAGTGGGCTGGACTGAATCAA 1511
Db |||||||
Qy 461 SerAlaSerCysProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsnGln 480
Db |||||||
Qy 1512 TGGATCTGTATAGATGAGTGTGTATGAGTGGGATAAACAATGTACAGACACATTTGGC 1571
Db |||||||
Qy 481 TrpIleCysIleAspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPheGly 500
Db |||||||
Qy 1572 AAAGAAGTAGTGTGGCCCTTCAGATGTTATTCTCACTTAATTCAAAGACTGATGA 1631
Db |||||||
Qy 501 LysGluValGluPheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAspVal 520
Db |||||||
Qy 1632 TCTGGAACCTGTGTATAGTATTCAGGATACACACAGTGTGAGCTGCAATCTCAG 1691
Db |||||||
Qy 521 SerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeuGln 540
Db |||||||
Qy 1692 TGCGAAAAATTAATATGTAATATGTAGTAAATTTTATTACAAATTTCCAAAGAGCCACT 1751
Db |||||||
Qy 541 CysGlyLysLeuIleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAlaThr 560
Db |||||||
Qy 1752 ATTTATTTATGCAACATAAGTGGACATCTGCAATCTGTGGAATTTGCCAGTATCAT 1811
Db |||||||
Qy 561 IleIleTyrAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAspHis 580
Db |||||||
Qy 1812 GCACAGCCCAAAAGATGTGATAAAGATGGAATCTTCTGCTTCAATTAAGTTGTC 1871
Db |||||||
Qy 581 AlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysValCys 600
Db |||||||
Qy 1872 AGGAATCAAGATGTGTGAGTCTTCTACTCTGCTTGTATGTTGCTACTGACAAATGTC 1931
Db |||||||
Qy 601 ArgAsnGlnArgCysValSerSerTyrLeuGlyTyrAspCysThrThrAspLysCys 620
Db |||||||
Qy 1932 AATGATAGGTGTATGCAATAACAAAAGCAGTGTCTGCTGCTTCAATTTACCT 1991
Db |||||||
Qy 621 AsnAspArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeuPro 640
Db |||||||
Qy 1992 CCAGATTGCTCAGTTCATCAGATCTATGGCTGTGGAGTATTCAGTGGCAATTTT 2051
Db |||||||
Qy 641 ProAspCysSerValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAsnPhe 660
Db |||||||

Qy 2052 CCACCTCTAGCTATPACAGCCAGACTCCCTCGAAAGCGCTACATGTGAGAACATTTACCAT 2111
Db |||||||
Qy 661 ProProValAlaIleProAlaArgLeuProGluArgTyrIleGluAsnIleTyrHis 680
Db |||||||
Qy 2112 TCCAACCAATGAGATGGCCATTTTCTTATTATTCATTCCTTCTTTATTATTCTGTGTA 2171
Db |||||||
Qy 681 SerLysProMetArgTrpProPhePheLeuPheIleProPhePheIlePheCysVal 700
Db |||||||
Qy 2172 CTGATTCCTTAATATGGTGAAGATTAAATTCCAAAGGAAAAATGCGAAGCTGAGGACTAT 2231
Db |||||||
Qy 701 LeuIleAlaIleMetValLysValAsnPheGlnArgLysIlePheGlnThrGluAspTyr 720
Db |||||||
Qy 2232 TCAGCGATGAGCAACCTGAAAGTGAGAGTGAACCTAAAGCG 2273
Db |||||||
Qy 721 SerSerAspGluGlnProGluSerGluSerGluProLysGly 734
Db |||||||
RESULT 3
ADB75186
ID ADB75186 standard; protein; 734 AA.
XX
AC ADB75186;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker protein.
XX
OS Prostate; cancer; cytostatic; gene therapy; marker.
XX
KW Homo sapiens.
XX
PN WO2003009814-A2.
XX
PD 06-FEB-2003.
XX
PF 25-JUL-2002; 2002WO-US023913.
XX
PR 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Schlegel R, Monahan JB, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
DR WPI; 2003-248033/24.
XX
PT New nucleic acid molecule, useful for diagnosing or treating prostate cancer.
XX
PS Disclosure; SEQ ID NO 10; 99pp; English.
XX
CC The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 734 AA;
XX
Alignment Scores:

Pred. No.: 0 Length: 734
Score: 3984.00 Matches: 734
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.07% Indels: 0
DB: 7 Gaps: 0

US-10-054-683-18 (1-2640) x ADB75186 (1-734)

QY 72 ATGTGGGTCTGTTCTGCTCAGCGGGCTCGCGGGCTCGCGATGAGCAGTAATTTTGAT 131
DB 1 MetTrpValLeuPheLeuLeuSerGlyLeuGlyLeuArgMetAspSerAsnPheAsp 20
QY 132 AGTTTACCTGTGCAAAATTTACAGTTCCGAGAGAAATACGGTCAATTAATAAGGAAGGAAAT 191
DB 21 SerLeuProValGlnIleThrValProGluLysIleArgSerIleIleLysGluGlyLe 40
QY 192 GAATCGCAGGCATCTCAAAATTTGTAATTTGAAGGGAACCATATATCTGTGTAATTAATG 251
DB 41 GluSerGlnAlaSerTyrLysIleValIleGluGlyLysProTyrThrValAsnLeuMet 60
QY 252 CAAAAAATCTTTTACCCCAATAATTTAGAGTTTACAGTTTACAGTTTACAGTTTACAGTTTAC 311
DB 61 GlnLysAsnPheLeuProHisAsnPheArgValTyrSerTyrSerGlyThrGlyLeMet 80
QY 312 AAACCACTGTGCAAGATTTTTCAGAAATTTCTGCCACTTACCAAGGCTATATTGAAGGTTAT 371
DB 81 LysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGlyTyr 100
QY 372 CCAAAATCTGTGGTGTGTAGTACACATGTACTGGACTCAGGGGGCTACTACAGTTTGAA 431
DB 101 ProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGlu 120
QY 432 AATGTTAGTTATGAATAGAACCCCTCGAGTCCTTTCAGTTGGCTTTGAACATGTAAATTTAC 491
DB 121 AsnValSerTyrGlyIleGluProLeuGluLysSerValGlyPheGluHisValIleTyr 140
QY 492 CAAGTAAACATAAGAAGCAGATGTTTCTCTTATATATGAAGAGGATATTGAATCAAGA 551
DB 141 GlnValLysHisLysLysAlaAspValSerLeuTyrAsnGluLysAspIleGluSerArg 160
QY 552 GATCTGTCCTTTAAATTTACAAAGCGCAGAGCCACAGCAAGATTTTGCAGATATATAGAA 611
DB 161 AspLeuSerPheLysLeuGlnSerAlaGluProGlnAspPheAlaLysTyrIleGlu 180
QY 612 ATGCATGTTATAGTTGAAAACAAATGTATATCATATGGGTCTGATACAACTGTTGTC 671
DB 181 MethisValIleValGluLysGlnLeuTyrAsnHisMetGlySerAspThrThrValVal 200
QY 672 GCTCAAAAAGTTTCCAGTTGATGGAATGCGAATGCTATTTTGTTCATTTTAATATT 731
DB 201 AlaGlnLysValPheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAsnIle 220
QY 732 ACAATATTCTGCTTCTCATGCGACTTGGATAGATGAATAATAAATTTGCACACCTGGA 791
DB 221 ThrIleIleLeuSerSerLeuGluLeuTrpIleAspGluAsnLysIleAlaThrThrGly 240
QY 792 GAAGCTAATGAGTTATTACACACATTTTAAAGATGGAACCATCTTATCTTGTGTTTACGT 851
DB 241 GluAlaAsnGluLeuLeuHisThrPheLeuArgTrpLysThrSerTyrLeuValLeuArg 260
QY 852 CCTCATGATGTGGCATTTTTCATCTGTTTACAGAGAAAGTCAAAATATTGTTGGTGCACAC 911
DB 261 ProHisAspValAlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAlaThr 280
QY 912 TTTCAGGGAAGATGTGTGATGCAAACTATGACAGAGGTGTTGTTCTGCGACCCAGAAC 971
DB 281 PheGlnGlyLysMetCysAspAlaAsnTyrAlaGlyGlyValValLeuHisProArgThr 300
QY 972 ATAGTCTGGAATCAGTTGAGTTATTTTACCTCAATATTAGCCTTAGTATCGGGATC 1031
DB 301 IleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyLe 320

QY 1032 ACTTATGATGACATTAACAATGCCAGTGTCTCAGGAGCTGTCTGCATTTATGAATCCAGAA 1091
DB 321 ThrTyrAspAspIleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnProGlu 340
QY 1092 GCAATTCATTTCACTGTGTGAAGATCTTTAGTAACATGCGAGCTTCGAGACTTTGCGACAT 1151
DB 341 AlaIleHisPheSerGlyValLysIlePheSerAsnCysSerPheGluLeuPheAlaHis 360
QY 1152 TTTATTTCAAAGCAGAAAGTCCCAGTGTCTTTCACAATCAGCCTCGCTTAGATCTCTTTTTC 1211
DB 361 PheIleSerLysGlnLysSerGlnCysLeuHisAsnGlnProArgLeuLeuAspProPhePhe 380
QY 1212 AAACAGCAGCAGTGTGTGTATGCAAGCTGGAACGAGAGAGAGTGTGACTGTGGG 1271
DB 381 LysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluGluCysAspCysGly 400
QY 1272 ACTGAACAGGATGTGCTCCCTTTATTTGGAGAAACATGCTGTGATATTGCGACATGTAGATT 1331
DB 401 ThrGluGlnAspCysAlaLeuIleGlyLysThrCysCysAspIleAlaThrCysArgPhe 420
QY 1332 AAAGCCGGTTCAAACCTGCTGAAGGACCATGCTGCGAAACCTGTCTATTATTCTCAAAA 1391
DB 421 LysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSerLys 440
QY 1392 GAAAGAAATGTGTAGGCTTCTTTGAAGAAATGCGACTCCCTGAAATATTGCAATGGATCA 1451
DB 441 GluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGlySer 460
QY 1452 TCTGCATCATGCCAGAAAACCACTATGTTTCAGACTCGGATCCGTGCGACTCAATCAA 1511
DB 461 SerAlaSerCysProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsnGln 480
QY 1512 TGGATCTGTATAGATGAGTTTGTATGAGTGGGATAAACAATGTACAGACACATTTGGC 1571
DB 481 TrpIleCysIleAspGlyValCysMetSerSerGlyAspLysGlnCysThrAspThrPheGly 500
QY 1572 AAAGAAGTAGATTGGCCCTTCAGAAATGTTTCTCACCTTAATTCAGAGACTGATGTA 1631
DB 501 LysGluValGluPheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAspVal 520
QY 1632 TCTGGAACCTGTGTATAAGTATTCAGGATACACAGATGTTGAAGCTGCAATCTGCAG 1691
DB 521 SerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeuGln 540
QY 1692 TCGGAAAAATTAATATGTAATATGTAAGTAAATTTTATTACAAATTTCCAAAGAGCCACT 1751
DB 541 CysGlyLysLeuIleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAlaThr 560
QY 1752 ATTATTTATGCCAACATAAGTGGACATCTCTGCAATGCTGTGGAATTTGCCAGTATCAT 1811
DB 561 IleIleTyrAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAspHis 580
QY 1812 GCACAGACCAAAAGATGTGTAATAAAGATGGAACCTTCTGTGGTTCAATAAGGTTTGC 1871
DB 581 AlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysValCys 600
QY 1872 AGGAATCAAAGATGTGTGAGTCTTCTCATCTTGGTTATGATTTGATCTACTGACAAATGC 1931
DB 601 ArgAsnGlnArgCysValSerSerSerTyrLeuGlyTyrAspCysThrThrAspLysCys 620
QY 1932 AATGATAGAGTGTATGCAATAACAAAGACATGTCTGCTAGTGTCTTCAATTTTACCT 1991
DB 621 AsnAspArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeuPro 640
QY 1992 CCAGATTGCTCAGTTCAATCAGATCTATGCGCTGTGGGAGTATTGACAGTGGCAATTTT 2051
DB 641 ProAspCysSerValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAsnPhe 660
QY 2052 CCACCTGTAGTATATACCAAGCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCAT 2111
DB 661 ProProValAlaIleProAlaArgLeuProGluArgTyrIleGluAsnIleTyrHis 680
QY 2112 TCCAAACCAATGAGATGGCCATTTTCTTATTCATCTTCTTTTATTATTCTGTGTA 2171


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Db 341 GluAlaIleHisPheSerGlyValLysIlePheSerAsnCysSerPheGluAspPheAla 360
QY 1149 CATTATTATTTCAAGCAGAGTCCAGTGTCTTCACAATCAGCTCGCTTAGATCTCTTTT 1208
Db 361 HisPheIleSerLysGlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPhe 380
QY 1209 TTCAACAGCAGACAGTGTGTGTAATGCAAGCTGGAAGCAGGAGAGTGTGACTGT 1268
Db 381 PheLysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluGluCysAspCys 400
QY 1269 GGCACCTGAACAGATGTGTGCCCTTATTGGAAACATGCTGTGATATTGCCACATGTAGA 1328
Db 401 GlyThrGluGlnAspCysAlaLeuIleGlyGluThrCysCysAspIleAlaThrCysArg 420
QY 1329 TTTAAAGCCGTTCAAACTGTCTGAAGGACCATGCTGCGAAACCTGCTATTATTATGTCA 1388
Db 421 PheLysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSer 440
QY 1389 AAAGAAAGAAATGTGTAGGCCCTTCTTTGAAGAAATGCGACCTCCCTGAATATTGCAATGGA 1448
Db 441 LysGluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGly 460
QY 1449 TCATCTGCATCATGCCAGAAAACCACTATGTCAGACTGGGCATCGGTGTGCACTGAAT 1508
Db 461 SerSerAlaSerCysProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsn 480
QY 1509 CAATGATCTGTATAGATGAGTTGTATGAGTGGGATAAACAATGTACAGACACATTT 1568
Db 481 GlnTrpIleCysIleAspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPhe 500
QY 1569 GCGAAAGAAAGTAGAGTTGGCCCTTCCAGAAATGTTATTCTCACCTTAATTCAAAGACTGAT 1628
Db 501 GlyLysGluValGluPheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAsp 520
QY 1629 GTATCTGGAAACTGTGTGATAAGTGATTACAGATATACACAGTGTGAGCTGACATCTG 1688
Db 521 ValSerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeu 540
QY 1689 CAGTGGGAAAATATATATTAATGTAAGTAAATTTTATTACAAATTCGAAGGCC 1748
Db 541 GlnCysGlyLysLeuIleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAla 560
QY 1749 ACTATTATTTATGCCAACATAAGTGACATCTCTGCATTCCTGTGGAATTTGCCAGTGAT 1808
Db 561 ThrIleIleTyrAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAsp 580
QY 1809 CATGCGACAGCCAAAGATGTGGATAAAGATGGAACCTTCTTGTGTTTCAAAATAGGTT 1868
Db 581 HisAlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysVal 600
QY 1869 TGCAGGAATCAAGATGTGTGAGTCTTCTCATCTTGGTTATCATTTCTACTACTGACAA 1928
Db 601 CysArgAsnGlnArgCysValSerSerSerTyrLeuGlyTyrAspCysThrThrAspLys 620
QY 1929 TGCAAATGATAGAGTGTATGCAATAACAAAGACCTGTCACTGTAGTGTCTCATATTTA 1988
Db 621 CysAsnAspArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeu 640
QY 1989 CTTCCAGATTGCTCAGTTCAATCAGATCTATGCGCTGTGGAGATATTGACAGTGGCAAT 2048
Db 641 ProProAspCysSerValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAsn 660
QY 2049 TTTTCCACCTGTAGTATATACAGCCAGACTCCCTGGAAGCGCTACATTGGACATTTAC 2108
Db 661 PheProProValAlaIleProAlaArgLeuProGluArgTyrIleGluAsnIleTyr 680
QY 2109 CATTCCAAACCAATGAGATGGCAATTTTCTTATTCAATTCCTTCTTTATTATTCTGT 2168
Db 681 HisSerLysProMetAlaGlyTrpProPhePheLeuPheIleProPhePheIleIlePheCys 700
QY 2169 GTACTGATTCCTAATGTTGAAAGTTAATTTCCAAAGGAAAAATGAGAACTGAGGAC 2228
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Db 701 ValLeuIleAlaIleMetValLysValAsnPheGlnArgLysLysTrpArgThrGluAsp 720
QY 2229 TATTCAAGCGATGAGCAACCTGAACGTGAGAGTGAACCTAAAGGG 2273
Db 721 TyrSerSerAspGluGlnProGluSerGluSerGluProLysGly 735
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RESULT 5

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ADB75182
ID ADB75182 standard; protein; 753 AA.
XX ADB75182;
XX 04-DEC-2003 (first entry)
XX Prostate cancer marker protein.
XX Prostate; cancer; cytostatic; gene therapy; marker.
XX Homo sapiens.
XX WO2003009814-A2.
XX 06-FEB-2003.
XX 25-JUL-2002; 2002WO-US023913.
XX 25-JUL-2001; 2001US-0307982P.
XX 22-AUG-2001; 2001US-0314356P.
XX 25-SEP-2001; 2001US-0325020P.
XX 12-DEC-2001; 2001US-0341746P.
XX 05-MAR-2002; 2002US-0362158P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
XX Hoerhn S, Kamatkar S, Wonsey AM, Giatt K, Zhao X, Anderson D;
XX WPI; 2003-248033/24.
XX New nucleic acid molecule, useful for diagnosing or treating prostate
XX cancer.
XX Claim 4; SEQ ID NO 6; 99pp; English.
```

The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX Sequence 753 AA;

Alignment Scores:			
Pred. No.:	0	Length:	753
Score:	3900.00	Matches:	720
Percent Similarity:	97.44%	Conservative:	4
Best Local Similarity:	96.90%	Mismatches:	13
Query Match:	81.32%	Indels:	6
DB:	7	Gaps:	1

US-10-054-683-18 (1-2640) x ADB75182 (1-753)

QY 45 TCCGGCTGGGACCCAGGACTTCAAGCCATGTGGGTCTTGTCTCTCAGCGGCTCGGC 104

CC polypeptides are used to identify modulators. A peptide, phosphopeptide, small organic molecule or an antibody is used to inhibit aberrant activity of a 56294 or 56629-expressing cell, located in a cancerous or pre-cancerous tissue. A compound that modulates the activity or expression of the polynucleotides are used to treat or prevent a disorder characterized by aberrant activity of a 56294 or 56629-expressing cell, in a subject. The present sequence represents the human 56294 protein

XX SQ Sequence 820 AA;

Alignment Scores:

Pred. No.: 1,01e-127 Length: 820
Score: 1530.00 Matches: 318
Percent Similarity: 57.84% Conservative: 132
Best Local Similarity: 40.87% Mismatches: 266
Query Match: 31.90% Indels: 62
DB: 6 Gaps: 20

US-10-054-683-18 (1-2640) x ABR39696 (1-820)

QY 6 CGCACTTCCAACTGCCCTGTAAACCAACTGCCCTTATTCGGCTGGGACCCAGGACTT 65
DB 22 ArgThrArgGlyCys-----TrpGlnProArgSer 31
QY 66 CAAGCCATGGGTCTGTTT---CTGCTCAGCGGCTCGCGGGCTCGGATGGAC--- 119
DB 32 ArgThrMetPheArgLeuTrpLeuLeuAlaGlyLeuCysGlyLeuAlaSerArg 51
QY 120 AGTAATTTTATGATGTTTACCTGTGCAAAATTACAGTTCCGGAGAAATACGGTCAATAATA 179
DB 52 ProGlyPheGlnAsnSerLeuLeuGlnIleValleProGluLysIleGlnThrAsnThr 71
QY 180 AAGGAAGGAATTGAA-----TGGCAGGCATCTACAAATTTGTAATGAAGGAAA 230
DB 72 AsnArgSerSerGluIleGluTrpGluGlnIleSerTyrIleProIleAspGluLys 91
QY 231 CCATATACCTGCAATTTAATGACAAAATTTTACCCCAATTTTAGAGTTTACAGT 290
DB 92 LeuTyrThrValHisLeuLysGlnArgTyrPheLeuAlaAspAsnProMetIleTyrLeu 111
QY 291 TATAGTGGCAGGAATATGAAACCACTTGACCAAGATTTTCAGAAATTTCTGCCACTAC 350
DB 112 TyrAsn---GlnGlySerMetAsnThrTyrSerSerAspIleGlnThrGlnCysTyrTyr 130
QY 351 CAAGGGTATATTGAAGTTATCCAAAATCTGTGTGATGGTTAGCACATGACTGCACTC 410
DB 131 GlnGlyAsnIleGluGlyTyrProAspSerMetValThrLeuSerThrCysSerGlyLeu 150
QY 411 AGGGCGTACTACAGTTTGAAATCTGTATGGAATAGAACCCCTGGAGCTTCAGTT 470
DB 151 ArgGlyIleLeuGlnPheGluAsnValSerTyrGlyIleGluProLeuGluSerAlaVal 170
QY 471 GCCTTTGAACATGTAATTTACCAAGTAAAAATAGAAAGCAGATGTTCTCTTATATAAT 530
DB 171 GluPheGlnHisValLeuTyrLysLeuLysAsnGluAspAsnAspIleAlaIlePheIle 190
QY 531 CAGAAGGATATTGAATCAAGA-----GATCTGCTCTTTAAATTAATCAAGCGCAGAG 581
DB 191 AspArgSerLeuLysGluGlnProMetAspAspAsnIlePheIleSerGluLysSerGlu 210
QY 582 CCACAGCAAGAT-----TTTGCAAGATATAGAAATGCATGTTATAGTTGAAACAA 635
DB 211 ProAlaValProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspIleThr 230
QY 636 TTGTATATCATATGGGCTGTATACAACTGTTCTCGCTCAAAAAGTTTTCAGTTGATT 695
DB 231 LeuTyrAspTyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluIleVal 250
QY 696 GGAATTGACGAATGCTATTGTTTTCATTTAATTAATTAATTAATTAATTAATTAATTAAT 755
DB 251 GlyLeuAlaAsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGlu 270
QY 756 CTTTGGATAGATGAAATAAAATTTGCAACCACTGGAGAAGCTAATGAGTTATTACACACA 815

DB 271 LeuTyrSerAspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuGlnLys 290
QY 816 TTTTAAAGTGAAGAAACATCTTATCTTGTGTTTAACTCTCTCATGATGTGGCATTTTACTT 875
DB 291 PheLeuGluTyrLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaIleTyrLeuLeu 310
QY 876 GTTTACAGAGAAAGTCAAATATTGTTGGTGCAACCTTTTCAAGGGAAGATGTGTGATGCA 935
DB 311 IleTyrMetAspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThr 330
QY 936 AACTATGTCAGGAGGTGTTTCTGCACCCAGAACCACTAAGTCTGGATCACTTGCAGTT 995
DB 331 ArgTyrSerAlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaVal 350
QY 996 ATTTTAGCTCAATTTATTGAGCCTTAGTAGTGGGATCACTTATGATGACATTAACAAATGC 1055
DB 351 IleValThrGlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCys 370
QY 1056 CAGTCTCAGGAGCTGCTGCATATATGAATCCAGAACCAATTCATTTCAAGTGTGTGAAG 1115
DB 371 GlnCysSerGluSerThrCysIleMetAsnProGluValGlnSerAsnGlyValLys 390
QY 1116 ATCTTTAGTAACTGCAGCTTCGAAGACTTTTGCAATTTTTCATTTTCAAGCAGAGTCCAG 1175
DB 391 ThrPheSerSerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLys 410
QY 1176 TGCTTCAATCAGCTCCTCGCTTAGATCTTTTTCACACAG---CAAGCAGTGTGTGGT 1232
DB 411 CysLeuGlnAsnAsnThrArg-----ProGlnLysLysSerProLysProValCysGly 428
QY 1233 AATGCAAGCTGGAAGCAGGAGGAGTGTGACTGTGGGACTGCAACAGGATTTGCGCCTT 1292
DB 429 AsnGlyArgLeuGluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly--- 447
QY 1293 ATTGGAGAACATCTGTGTATTTGGCCATATTTGACATGTAGATTTTAAAGCCGTTCAAACTGTGCT 1352
DB 448 ---ProAlaSerCysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyr 466
QY 1353 GAAGGACCATGCTCGCAAAACTGTCTATTATGTCTCAAAAGAAAGATGTGTAGGCT--- 1409
DB 467 LysGlyLeuCysCysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLys 486
QY 1410 TCCTTTGAAGAAATGCACCTCCCTGAAATATTTGCAATGATGATCTCTCATCATGCCAGAA 1469
DB 487 AlaHisProGluCysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyPro 506
QY 1470 AACCACTATGTTGAGCTGGGCATCCGTGTGAGCTGAATCAATGGATCTGTATAGATGA 1529
DB 507 AspIleThrLeuIleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGly 526
QY 1530 GTTTGTATGATGGGGATAAACAATGTACAGACACATTTGGCAAGAGTACAGTTGGC 1589
DB 527 AspCysHisAspLeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAla 546
QY 1590 CCTTCAGAAATGTTATTTCTCACCTTAATTCAAAGACTGATGATCTGGAACCTGTGTATA 1649
DB 547 ProPheAlaCysTyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArg 566
QY 1650 AGT---GATTGAGGATACACAGTGTGAAGCTGCAATCTCGAGTGGCGGAAATTAATA 1706
DB 567 AspArgAsnAsnLysTyrValPheCysGlyTyrPheAsnLeuIleCysGlyArgLeuVal 586
QY 1707 TGTAAATATGAGTAAATTTTATACAAATTTTCAAGAGCCACTATTATTATTCGCAAC 1766
DB 587 CysThrTyrProThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPhe 606
QY 1767 ATAAGTGGACATCTCTGCAATGCTGTGAAATTTGCGAGTATGATCATGCAGACAGCCAAAG 1826
DB 607 ValArgSerValCysIleThrValAspTyrLysLeuProArgThrValProAspPro 626
QY 1827 ATGTGGAATAAGATGGAACCTCTTGTGTTCAATAATAGTTTGCAGGAATCAAGATGT 1886
DB 626

QY 420 CTACAGTTTCAGAAATGTTAGTATGGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAA 479
DB 121 LeuGlnPheGluAsnValSerTyrGlyLeuProLeuGluSerAlaValGluPheGln 140
QY 480 CATGTATTTACCAAGTAAACATATAAGAACAGAGATGTTTCCTTATATATATGAGAAGGAT 539
DB 141 HisValLeuTyrLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer 160
QY 540 ATTGAATCAGA-----GATCTGCTCTTTAAATTAACAAAGCCAGAGCCACAGCAA 590
DB 161 LeuLysGluGlnProMetAspAsnIlePheIleSerGluLysSerGluProAlaVal 180
QY 591 GAT-----TTTGCAAGATATAGAAATGCATGTTATAGTTGTAAGAAACAAATTTGATAT 644
DB 181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValAspLysThrLeuTyrAsp 200
QY 645 CATATGGGTCTGATACAACTGTTGCGTCAAAAAGTTTCCAGTTGATGAGTTGAGC 704
DB 201 TyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluIleValGlyLeuAla 220
QY 705 AATGCTATTTTCTTTCATTAATATACAAATTTATCTCTCTCTCATGAGCTTTGGATA 764
DB 221 AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGluLeuTyrSer 240
QY 765 GATGAAATATAAATTCACCACTGAGAGAGCTTAATGAGTTTATACACATTTTAAAGA 824
DB 241 AspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuGlnLysPheLeuGlu 260
QY 825 TGGAAACATCTTCTCTTCTGCTCTCATGATGCGCATTTTACTTGTTCACAGA 884
DB 261 TrpLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaTyrLeuLeuIleTyrMet 280
QY 885 GAAAGTCAAAATATGTTGCTGCAACCTTTCAAGGGAAGATCTGTGATGCAAACTATCCA 944
DB 281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
QY 945 GGAGTGTGTTCTGACCCCAAGAACCAATGCTGGAATCACTTTCAGTTTATTTAGCT 1004
DB 301 AlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
QY 1005 CAATTTATTGAGCTTAGTATGGGATCACTTATGATGATGATTAACAAATGCCAGTCTCA 1064
DB 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCysGlnCysSer 340
QY 1065 GGAGCTGTCTCATATGATCAAGCAATTCATTTTCAGTGGTGTGAAGATCTTTAGT 1124
DB 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
QY 1125 AACTGCAGCTTCCAGAGCTTGCACATTTTATTTCAAAAGCAGAGTCCAGTGTCTCAC 1184
DB 361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
QY 1185 AATCAGCTCGCTAGATCTCTTTTCAACAGCAGCAGTGTGTGTTAATGCAAGCTG 1244
DB 381 AsnLysProGlnMetGlnLys----LysSerProLysProValCysGlyAsnGlyArgLys 399
QY 1245 GAACAGGAGAGGAGTGTGATGTGGGACTGAACAGGATTTGTCCTTTATGGAGAAACA 1304
DB 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
QY 1305 TGCTGTGATATTGCCACATGTAGATTTAAACCCGTTCAAACTGTGCTGAAGACCATGC 1364
DB 418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
QY 1365 TCGAAAACTGCTATTTATTCATCAAAAGAAAGATGTGTAGGCTCT---TCCTTTGAAGAA 1421
DB 438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
QY 1422 TGGCACTCCCTCGAATTTGCAATGAGATCATCTGCATCATGCCAGAAACCACTATGTT 1481
DB 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477

QY 1482 CAGACTGGGCATCCGTGTGGAGTCAATCAATGGAATCTGTATAGATGGAGTTTGTATGAGT 1541
DB 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGlyAspCysHisAsp 497
QY 1542 GGGGATAAACAATGTACACAGACACATTTGGCAAGAAAGTAGAGTTTGGCCCTTCAGATGT 1601
DB 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
QY 1602 TATTCTACCTTAATTTCAAGACTGATGATCTCGAAACTGTGTATATAAGT---GATTCA 1658
DB 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
QY 1659 GGATACACACAGTGTGAAGCTGACAAATCTGCAGTGGCGAAATTAATATGTAATATGTA 1718
DB 538 LysTyrValPheCysGlyTrpArgAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
QY 1719 GGTAAATTTTATTACAAATTTCCAAAGAGCCACTATTATTATGCAACATTAAGTGGACAT 1778
DB 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
QY 1779 CTCTGCATTTGCTGTGGAATTTGCCAGTGCATGCACAGCCAGCAAAAGATGTGGATAAAA 1838
DB 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
QY 1839 GATGAACTTCTTGTGTTCAAATAGGTTTGCAGGAATCAAGATGTGTGAGTTCTTCA 1898
DB 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
QY 1899 TACTTG-----GGTTATGATTGTACTACACAAATGCAATGATGATAGAGTGTATGC 1949
DB 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
QY 1950 AATAACAAAAGCACTGTCTACTGTAGTCTTCATATTTACTCCAGATGTCTCAGTTCAA 2009
DB 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProAsnCysGlnIleArg 656
QY 2010 TCAGATCTATGGCTGTGGGAGTATT-----GACAGTGCSCAATTTTCCACCT 2057
DB 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle 671
QY 2058 GTAGCTATACAGCCAGACTCCCTGAAAGCGCTACATTTAGAGAACATTTTACCATTCCAAA 2117
DB 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTTCTTCTTATTTATTTCTGTGTA 2171
DB 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATGTCTATATGTTGAAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT 2231
DB 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
QY 2232 TCAAGCGATGACCACTGAAAGTGAAGTGAACCTTAAGGG 2273
DB 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726
RESULT 10
ABU80783
ID ABU80783 standard; protein; 787 AA.
XX
AC ABU80783;
XX
XX 23-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #45.
XX
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX
XX Homo sapiens.
XX
PN US2003036635-A1.
XX

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PD 20-FEB-2003.
XX
PF
PR 28-AUG-2002; 2002US-00230163.
XX
PR 25-JUL-2000; 2000US-0220638P.
XX
PR 01-JUN-2001; 2001HO-US017800.
PR 29-JUN-2001; 2001HO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-342045/32.
DR N-PSDB; ACA66885.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for the manufacture of a medicament for diagnosing or treating
XX tumor.
XX
XX Claim 11; Fig 90; 314pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
XX useful in diagnostic assays for PRO, by detecting its expression in
XX specific cells, tissues or serum, and for affinity purification of PRO
XX from recombinant cell culture or natural sources. ABUS0739-ABUS08060
XX represent the human PRO polypeptides of the invention. Note: The sequence
XX data for this patent was obtained in electronic format directly from the
XX USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
XX Sequence 787 AA;
SQ
Alignment Scores:
Pred. No.: 3,08e-127 Length: 787
Score: 1524.50 Matches: 310
Percent Similarity: 58.89% Conservative: 134
Best Local Similarity: 41.11% Mismatches: 259
Query Match: 31.79% Indels: 51
DB: 6 Gaps: 18
US-10-054-683-18 (1-2640) x ABUS0783 (1-787)
QY 72 ATGTGGTCTGTTCTGCTCAGCGGCTCGCGGGCTCGCGATGAC---AGTAATTTT 128
DB 4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21
QY 129 GATAGTTTACCTGTGCAAAATTACAGTTCCGAGAAATACGGTCAATAATAAGGAAGGA 188
DB 22 GlnAsnSerLeuLeuGlnIleValIleProGluLysIleGlnThrAsnThrAsnAspSer 41
QY 189 ATTGAA-----TCGACGGCATCTACAAAATTGTAAATTGAAGGGAACCATATACT 239
DB 42 SerGluIleGluTyrGluGlnIleSerTyrIleIleProIleAspGluLysLeuTyrThr 61
QY 240 GTGAATTAATGCAAAAATACTTTTACCCCATTAATTTAGAGTTTACAGTTTATAGTGGC 299
DB 62 ValHisLeuLysGlnArgTyrPheLeuAlaAspAsnPheMetIleTyrLeuTyrAsn--- 80
QY 300 ACAGGAATTATGAACACCTTGACCAAGATTTCAGAAATTTCTGCCACTACCAAGGGTAT 359
DB 81 GlnGlySerMetAsnThrTyrSerSerAspIleGlnThrGlnCysTyrTyrGlnGlyAsn 100
QY 360 ATTGAAGTTTATCAAAATCTGGTGATGGTTAGCACATGTACTGTGACTCAGGGCGGTA 419
DB 101 IleGluGlyTyrProAspSerMetValThrLeuSerThrCysSerGlyLeuArgGlyIle 120
QY 420 CTTACAGTTGAAATGTTAGTTATGGAATAGAACCCCTGAGTCTTCAGTTGGCTTTGAA 479

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121 LeuGlnPheGluAsnValSerTyrGlyIleGluProLeuGluSerAlaValGluPheGln 140
480 CATGTAAATTTACCAAGTAAACATAAGAAAGCAGATGTTTCCCTTATATATAGAAAGGAT 539
141 HisValLeuTyrLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer 160
540 ATTGAATCAAGA-----GATCTGTCTCTTTAAATTACAAAGCCGACGACCCACAGCAA 590
161 LeuLysGluGlnProMetAspAspAsnIlePheIleSerGluLysSerGluProAlaVal 180
591 GAT-----TTTGCAAAAGTATATAGAAATGTCATGTTATAGTTGAAAAACAATGTATAT 644
181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspLysThrLeuTyrAsp 200
645 CATATGGGCTCTGATACAACTGTTGCGCTCAAAAAGTTTCCAGTTGATGATGACG 704
201 TyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluIleValGlyLeuAla 220
705 AATGCTATTTTGTTCATTATATACATTAATATTCTGCTTCATTGAGCTTTGGATA 764
221 AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGluLeuTrpSer 240
765 GATGAAAAATAAAATTGCAACCACTGGAGAAAGCTAAATGAGTTATTACACACATTTTAA 824
241 AspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuLeuGlnLysPheLeuGlu 260
825 TGGAAACATCTTATCTGTTTACGTCCTCATGATGTCGCACTTTTACTTTGTTACAGA 884
261 TrpLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaTyrLeuLeuIleTyrMet 280
885 GAAAGTCAATATATGTTGTCACACTTTCAAGGGAAGATGTGTGATGCAAACTATGCA 944
281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
945 GGAGGTGTTGTTCTGCACCCAGAACCACTAAGTCTGCAATCACTTCAGTATTATTAGCT 1004
301 AlaGlyValAlaLeuLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
1005 CAATTATTGAGCCTTAGTATGGGGATCACTTATGATGACATTAACAAATCCAGTGTCTCA 1064
321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCysGlnCysSer 340
1065 GGAGCTGTCTGCATTAATGAATCCAGAAAGCAATTCATTTCAGTGTGTGAGATCTTTAGT 1124
341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
1125 AACTGCAGCTTCGAAGACTTTGCACATTTTATTTTCAAGCAGAAAGTCCCAAGTCTTTCAC 1184
361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
1185 AATCAGCCTCGCTTAGATCCCTTTTTCAAAACAGACAGCAGTGTGTGTTATATGCAAGCTG 1244
381 AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
1245 GAAGCAGGAGAGAGAGTGTGACTGTGGGACTGAACAGAGATTGTGCCCTTATTGGAGAAACA 1304
400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
1305 TGCTGTGATATTGCCACATGTAGATTAAAGCCGGTTTCAAACTGTCTGAGAGGCCATGC 1364
418 CysAspAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
1365 TGGCAAAACTGTCTATTATTATGTCAAAAGAAAGAAATGTGTAGGCT---TCCTTTGAAGAA 1421
438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
1422 TGGCACTCTCCCTGAATATTGCAATGATCATCTGCATCATCTGCCAGAAACCATATGTT 1481
458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
1482 CAGACTGGGCATCCGTGTGACTGTAATCAATGATCTGTATAGATGGAGTTTGTATGAGT 1541
478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGlyAspCysHisAsp 497

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QY 1542 GGGGATAAACAATGTACAGACACATTTGGCAAGAGTAGAGTTGGCCCTTCAGAAATGT 1601
 Db 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
 QY 1602 TATTCTCAGCTTAATTTCAAGACTGATGTATCTCGGAAACTGTGGTATATAAGT---GATTCA 1658
 Db 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnGlyArgAspArgAsnAsn 537
 QY 1659 GGATACACACAGCTGCAAGCTGACATCTGCGATGCGGAAATTAATATGTAATATGTA 1718
 Db 538 LysTyrValPheCysGlyTrpArgAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
 QY 1719 GGTAATATTTTATTACAAATTCACAGAGCCACTATTATTATTCGCAACATAGTGACAT 1778
 Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
 QY 1779 CTCTGCAATTCGTGGAAATTCGCCAGTATCATGCAGACAGCAAAAGATGTGATAAAA 1838
 Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
 QY 1839 GATGGAACCTCTGTGGTTCAATTAAGGTTTCAGGAATCAAGATGTGTGATTCCTCA 1898
 Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
 QY 1899 TACTTG-----GGTTATGATTGTACTGACAAATGCAATGATAGAGGTGTATGC 1949
 Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
 QY 1950 AATAACAAAGCACTGTCAGTGTAGTGTCTCATTTATCTCCAGATGTCAGTTCAA 2009
 Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProProAsnCysGlnIleArg 656
 QY 2010 TCAGATCATGCGCTGTGGGAGTATT-----GACAGTGGCAATTTCCACCT 2057
 Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
 QY 2058 GTAGCTATACAGCCAGACTCCCTGAAAGCGCTACATTTGAGAACATTTACCATTCACAA 2117
 Db 672 -----MetGluArgAlaSerGlyLysThr 679
 QY 2118 CCAATGAGATG-----CCATTTTCTTATTCATTCCTCTTCTTATTTATTTCTGTGTA 2171
 Db 680 GluAsnThrTrpLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
 QY 2172 CTGATGCTGCTAATGTTGTAAGTTAAATTTCCAAAGGAAATAATGGAGAACTGAGGACTAT 2231
 Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
 QY 2232 TCAAGCGATGAGCACTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2273
 Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 11

ABO33749

ID ABO33749 standard; protein; 787 AA.

XX ABO33749;

AC ABO33749;

XX 17-SEP-2003 (first entry)

DT 17-SEP-2003 (first entry)

XX 17-SEP-2003 (first entry)

XX 17-SEP-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO21340.

KW Human; secreted and transmembrane protein; PRO; cytostatic;

KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;

KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;

KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW liver tumour; bone disorder; cartilage disorder; sports injury;

KW arthritis; wound.

OS Homo sapiens.

XX

PN US2003045687-A1.
 XX 06-MAR-2003.
 XX 12-AUG-2002; 2002US-00218631.
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-512315/48.
 DR N-PSDB; ACD68637.
 XX New genes, and its encoded secreted and transmembrane polypeptides,
 useful for stimulating tumor Necrosis Factor alpha, or chondrocyte or
 pericyte proliferation, especially for treating lung tumors, arthritis or
 wounds in a mammal.
 Claim 11; Fig 90; 314pp; English.
 The invention describes an isolated nucleic acid molecule comprising a
 sequence with at least 80% identity to: (a) a nucleotide encoding any of
 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 fully defined in the specification; or (b) any of 122 nucleotide
 sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 specification; or the full length coding sequence of any these 122
 nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 particularly useful for detecting tumours (e.g. lung tumour, colon
 tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
 in a mammal, for stimulating the release of TNF-alpha from human blood,
 for stimulating the proliferation or differentiation of chondrocyte
 cells, for stimulating proliferation of pericyte cells, or for modulating
 normal human dermal fibroblast proliferation. The PRO nucleic acid or
 polypeptide is also useful for treating tumours or various bone and/or
 cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 PRO polypeptides are useful in drug screening, particularly as targets
 for therapeutic intervention in these diseases, and in the diagnostic
 determination of the presence of these diseases. The PRO polypeptides are
 also useful as molecular weight markers, or for chromosome
 identification. The PRO genes are useful as hybridisation probes, or for
 screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 also be used in gene therapy, particularly for replacing a defective
 gene. This is the amino acid sequence of a novel human secreted and
 transmembrane PRO polypeptide
 Sequence 787 AA;
 Alignment Scores:
 Pred. No.: 3,08e-127 Length: 787
 Score: 1524.50 Matches: 310
 Percent Similarity: 58.89% Conservative: 134
 Best Local Similarity: 41.11% Mismatches: 259
 Query Match: 31.79% Indels: 51
 DB: 6 Gaps: 18
 US-10-054-683-18 (1-2640) x ABO33749 (1-787)
 QY 72 ATGTGGTCTTGTCTCTCAGCGGCTCGCGGCTCGCGATGGAC---AGTAATTTT 128
 Db 4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21
 QY 129 GATAGTTTACCTGTCAATTTACAGTTCCGGAGAAATACCGTCAATAATAAGGAAGGA 188
 Db 22 GlnAsnSerLeuGlnIleValIleProGlyLysIleGlnThrAsnThrAsnAspSer 41
 QY 189 ATTGAA-----TCGAGGCATCTCAGAAATTTGTAATTGAAGGAACCATATACT 239

Db 42 SerGluLeuGluTyrGluGlnIleSerTyrIleIleProIleAspGluLysLeuTyrThr 61
QY 240 GTGAATTAATGCAAAAAAATTTTACCCCATAAATTTTAGAGTTTACAGTTATAGTGGC 299
Db 62 ValHisLeuLysGlnArgTyrPheLeuAlaAspAsnPheMetIleTyrLeuTyrAsn--- 80
QY 300 ACAGGAATTAAGAACACCTGACCAAGATTTTCAGAAATTTTCAGAAATTTTCAGCACTACCAAGGGTAT 359
Db 81 GlnGlySerMetAsnThrTyrSerSerAspIleGlnThrGlnCysTyrTyrGlnGlyAsn 100
QY 360 ATTGAAGGTTATCCAAAATCTGTGGTGATGCTGTAGCACATGTACTGGACTCAGGGCGTA 419
Db 101 IleGluGlyTyrProAspSerMetValThrLeuSerThrCysSerGlyLeuArgGlyIle 120
QY 420 CTACAGTTTCAAAATGTTAGTATGAATAAGAACCCCTGGAGTCTTCAGTTGGCTTTGAA 479
Db 121 LeuGlnPheGluAsnValSerTyrGlyIleGluProLeuGluSerAlaValGluPheGln 140
QY 480 CATGTAATTTACCAAGTAACATAAGAACGAGATGTTTCTTATATATATAGAAAGGAT 539
Db 141 HisValLeuTyrLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer 160
QY 540 ATTGAATCAAGA-----GATCTCTCTTAAATTAACAAGCCGACAGCCACACCAA 590
Db 161 LeuLysGluGlnProMetAspAspAsnIlePheIleSerGluLysSerGluProAlaVal 180
QY 591 GAT-----TTTCAAAAGTATATAGAAATCATGTTATAGTTGAAACAAATTTGATAAT 644
Db 181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspLysThrLeuTyrAsp 200
QY 645 CATATGGGTCGATCAACCTGTGTGCGCTCAAAAAGTTTTCAGTTGATGGATTGACG 704
Db 201 TyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluValGlyLeuAla 220
QY 705 AATGCTATTTTCTTTCATTAATATATACAAATTTATCTGCTTCATTTGGAGCTTGGATA 764
Db 221 AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuLeuLeuTrpSer 240
QY 765 GATGAAAAATAAATTCGACCACTCGAGAGAACTAATGAGTTATACACACATTTTAAAGA 824
Db 241 AspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuGlnLysPheLeuGlu 260
QY 825 TGAATAACATCTTATCTGTTTACGTCCTCATGATGGCATTTTACTTTGTTTACAGA 884
Db 261 TrpLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaTyrLeuLeuIleTyrMet 280
QY 885 GAAAAGTCAAATTAATGTTGGTGCACCTTTCAAGGAGAGATGCTGATGCAAACTATGCA 944
Db 281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
QY 945 GGAAGGTGTTCTTCGACCCCGAAGCAATCAAGTCTGGAATCACTTGCAAGTTATTTAGCT 1004
Db 301 AlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
QY 1005 CAATTAATGACCTTAGTATGGGATCATCTTATGATGACATTAACAAATCCAGTGTCTCA 1064
Db 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCysGlnCysSer 340
QY 1065 GGAGCTGTCGATTAATGAAATCAGAACCAATTCATTTACGTGGTGTGAGATCTTAGT 1124
Db 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
QY 1125 AACTGCACTTCGAAGACTTTGCACATTTTATTTTCAAGCAGAAAGTCCCAAGTCTTCAC 1184
Db 361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
QY 1185 AATCAGCTCGCTTAGATCTCTTTTCAACAGCAAGCAGATGCTGTGTAATGCAAAAGCTG 1244
Db 381 AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
QY 1245 GAAGCAGGAGAGAGTGTGATGCTGGGACTGAACAGGATTTGCCCTTATTTGGAGAAACA 1304
Db 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417

RESULT 12

ABU82092

ID ABU82092 standard; protein; 787 AA.

XX

QY 1305 TGCTGTGATATTGCCACATGTAGATTAAAGCCGGTTCAAACCTGCTGCTGAAGGACCAATGC 1364
Db 418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
QY 1365 TGGCAAAACCTGCTATTATATGTCAAAGAAAGAAAGTGTAGGCT---TCTTTTGAAGAA 1421
Db 438 CysLysAspCysGlnLeuLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
QY 1422 TGGGACTCTCCCTGAATATTGCAATGATCATCTGCATCATCTGCCAGAACCACTATGTT 1481
Db 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
QY 1482 CAGACTGGGCATCCGTGTGGACTGAATCAATCGATCTGTATAGATCGAGTTTGTATGAGT 1541
Db 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGlyAspCysHisAsp 497
QY 1542 GGGGATAAACAATGTATACACACATTTGGCAAGAAGTAGAGTTTGGCCCTTCAGATGT 1601
Db 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
QY 1602 TATTCTCACCTTAATTAAGACTGATGTATCTGGAACCTGTGCTATAAGT---GATTCA 1658
Db 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
QY 1659 GGATACACACAGTGTGAAGCTGCAATCTCCAGTGGCGAAAATTAATATGTAATATGTA 1718
Db 538 LysTyrValPheCysGlyTrpArgAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
QY 1719 GGTAATTTTATTACAAATTCAGAGCCACTATTATTATGCCAACATAAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
QY 1779 CTCGTGATTCGTCTGGAATTTGCCAGTGCATCATGCAGACAGCCAAAGAGTGGATAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
QY 1839 GATGAACTCTTCTGTGGTTCAAATAAGGTTTGCAGGAATCAAGAGATGTGTGAGTTCTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
QY 1899 TACTTG-----GGTTATGATTTGCTACTGACAAATGCAATGCAATAGAGTGTATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
QY 1950 AATAACAAAAGCAGCTGCTAGTCTGCTTTCATATTATCTCCAGATTCCTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProAsnCysGlnIleArg 656
QY 2010 TCAGATCTATGGCTGTGGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
QY 2058 GTAGCTATACAGCCAGACTCCCTGAAAGCGCTACATTGAGAACACATTACCATTCCTCAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATCAGATGG-----CCATTTTCTTATTCTTCCTTTCTTTTATTCTGCTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATTGCTATATGTTGAAGTTAATTTCCAAAGGAAAAAATGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysIleTyrPheAlaLysGlu--- 714
QY 2232 TCAAGCGATGAGCAACTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 12

ABU82092

ID ABU82092 standard; protein; 787 AA.

XX

QY	1245	GAAGCAGAGAGAGTGTGACTGTGGAGCTGAACAGGATTGTGCCCTTATTGGAGAAACA	1304
DB	400	GlulysAsnGluileCysAspCysgLyThrGluAlaGlnCysgLy-----ProAlaSer	417
QY	1305	TGCTGTGATATGCCACATGTAGATTAAAGCCGGTTCAAACCTGTCTGCTGAAGGACCATTGC	1364
DB	418	CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyLysGlyLeuCys	437
QY	1365	TGCGAAACACTCTCTATTATGTCTCAAAAGAAGATGTGTAGGCCT---TCTTTTGAAGAA	1421
DB	438	CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu	457
QY	1422	TGGACCTCCTCGAATATTCGAATGGATCATCTGCATCATGCCAGAAAAACCATGTATT	1481
DB	458	CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu	477
QY	1482	CAGACTGGGCATCGCTGTGGACTGAAATCAATGGATCTGTATAGATGAGTTTGTATGAGT	1541
DB	478	IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyLysAspGlyAspCysHisAsp	497
QY	1542	GGGGATAAACAATGTACAGACACATTTGGCAAGAAGTAGAGTTTGGCCCTTCAGAAATGT	1601
DB	498	LeuAspAlaArgCysGluSerValPhePheGlyLysGlySerArgAsnAlaProPheAlaCys	517
QY	1602	TATTCTCACCTTAATTCAAAGACTGATGTATCTGGAACCTGTGGTATAAGT---GATTCA	1658
DB	518	TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn	537
QY	1659	GGATACACACAGTGTGAAGCTGACAAATCTGCAGTGGCGAAAAATTAATATGTAAATATGTA	1718
DB	538	LysTyRValPheCysGlyTyrPArgAsnLeuIleCysGlyArgLeuValCysThrTyRPro	557
QY	1719	GGTAAATTTTATPACAAATTCCAAGAGCCACTATTATTATGCCAACATAAGTGGACAT	1778
DB	558	ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer	577
QY	1779	CTCTGCACTCTGTGGAAATTTGCCAGCTGATCATCCAGACACGCCAAAGATGTGGATAAAA	1838
DB	578	ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys	597
QY	1839	GATGGAAACTTCTTGCTGTTCAATAAGCTTTGCAGGAATCAAGAGATGTGAGTCTTCTTCA	1898
DB	598	AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg	617
QY	1899	TACTTG-----GGTTATGATGTACTACTGACAAATGCAATGATGAGGTGATATGC	1949
DB	618	IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys	636
QY	1950	AATAACAAAAGCACTCTCACTAGTGCCTTCATATTACTCCAGATTCTCGATTCAA	2009
DB	637	AspSerArgAsnLysCysHisCysSerProGlyTyrLysProProAsnCysGlnIleArg	656
QY	2010	TCAGATCTATGGCCTGTGTGGAGTATT-----GACATGGTCAATTTTCCACCT	2057
DB	657	Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle-----	671
QY	2058	GTAGCTATACAGCCAGACTCCCTGGAAGGGCGTACATTGAGAACAATTTACCATCCAAA	2117
DB	672	-----MetGluArgAlaSerGlyLysThr	679
QY	2118	CCAATGAGATGG-----CCATTTTCTTATTCAATCTCTTATTATTATTTCTGTGTA	2171
DB	680	GluAsnThrTrpLeuLeuGlyPheIleuIleAlaLeuProIleuIleVal-----	696
QY	2172	CTGATTCCTATAATGGTGAAGTTTAAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT	2231
DB	697	---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu---	714
QY	2232	TCAAGCGATGAGCAACTGAAAGTGAGAGTGAACTTAAGGG	2273
DB	715	-----GluGluPheProSerSerGluSerLysSerGluGly	726

RESULT 13	
ABUJ72272	
ID	ABUJ72272 standard; protein; 787 AA.
XX	
AC	ABUJ72272;
XX	
DT	06-NOV-2003 (first entry)
XX	
DE	Human PRO21340 protein.
XX	
KW	PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
KW	differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX	
OS	Homo sapiens.
XX	
FN	US2003050448-A1.
XX	
PD	13-MAR-2003.
XX	
FF	28-AUG-2002; 2002US-00230414.
XX	
PR	01-JUN-2001; 2001WO-US017800.
PR	29-JUN-2001; 2001WO-US021066.
PR	09-APR-2002; 2002US-00119480.
XX	
FA	(GETH) GENENTECH INC.
XX	
Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;	
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX	
DR	WPI: 2003-521818/49.
DR	N-PSDB; ABT44270.
XX	
PT	New nucleic acid encoding for a PRO protein, useful for the manufacture
PT	of a medicament for diagnosing or treating tumors or for measuring or
PT	detecting expression of an associated gene.
XX	
PS	Claim 11; Fig 90; 315pp; English.
XX	
CC	The invention relates to a novel isolated nucleic acid encoding a fully
CC	defined PRO polypeptide. The molecules of the invention may be useful for
CC	stimulating proliferation or gene expression in pericyte cells or the
CC	release of TNF-alpha from human blood. Other possible uses include the
CC	stimulation or inhibition of chondrocyte proliferation or
CC	differentiation, the stimulation of human dermal fibroblast cell
CC	proliferation and the detection of the presence of a tumour within a
CC	mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC	of a medicament for diagnosing or treating a tumour within a mammal or
CC	for measuring or detecting the expression of an associated gene, as well
CC	as during gene therapy. The current sequence is that of the human PRO
CC	protein of the invention
XX	
SQ	Sequence 787 AA;
Alignment Scores:	
Pred. No.:	3,08e-127 Length: 787
Score:	1528.50 Matches: 310
Percent Similarity:	58.89% Conservative: 134
Best Local Similarity:	41.11% Mismatches: 259
Query Match:	31.79% Indels: 51
DB:	6 Gaps: 18
US-10-054-683-18 (1-2640) x ABUJ72272 (1-787)	
Qy	72 ATGTGGGTCTGTGTTCTGCTCAGCGGCTCGCGGGCTGGCGATGGAC---AGTAATTTT 128
.	::: :::
Db	4 LrpLeu-----LeuLeuAlaGlyLeuLeuAlaSerArgProGlyphe 21
Qy	129 GATAGTTTACTGTGCAATTTACAGTTCCGAGAAATACGGTCAATTAATAAGGAAGA 188
.	::: :::
Db	22 GlnAsnSerLeuLeuGlnIleValleProGlnIlystleGlnThrAsnThrAsnAspSer 41

Db 418 CysCysAspPheArgThrCysValLeuLysAspGlyValAlaLysCysTyrLysGlyLeuCys 437
QY 1365 TGGAAACCTGCTCTATTTATGTCARAAAGAAAGTGTAGGCCT---TCCTTTGAAGAA 1421
Db 438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
QY 1422 TCGACCTCCCTCCATATTTGCAATGATGATCATCTGTCATCATGCCAGAAACCACTATGTT 1481
Db 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
QY 1482 CAGACTGGGCATCCGTGGACTGCAATCAATGATCTGTATAGATGGAGTTTGTATGAGT 1541
Db 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGlyAspCysHisAsp 497
QY 1542 GGGGATAAATGATACACACATTTGGCAAGAGTAGACTTTGGCCCTTCAGAAATG 1601
Db 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
QY 1602 TATCTCACCTTAATTCAAAGACTGATGTATCTGGAACCTGTGGTATAAGT---GATTCA 1658
Db 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
QY 1659 GGATACACACAGTGTGAAGTCAATCTGCAGTCGGGAAATTAATATGTAATATGTA 1718
Db 538 LysTyrValPheCysGlyTyrPargAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
QY 1719 GGTAAATTTTATTACAAATTCAGAGCCACTATTATTATTTGCAACATTAAGTGCACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
QY 1779 CTCTGCATTTGCTGGAAATTTGCCAGTGATCATGCAGACAGCCAAAGATGTGGATAAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
QY 1839 GATGAACTTCTGGGTTTCAATTAAGCTTTCAGGAATCAAGATGTGTAGTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
QY 1899 TACTTG-----GGTTATGATTGTACTACTGACAAATCAATGATAGAGGTGTATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
QY 1950 AATACAAAAGCACTGCTACTGTAGTCTTCATATTTACTCCAGATTCCTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProAsnCysGlnIleArg 656
QY 2010 TCAGATCTATGCTGCTGGTGGAGTATT-----GACATGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
QY 2058 GTAGCTATACAGCCAGACTCCCTGAAAGCGCTACATTTGAGAACATTTTACCATTCCAAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTCCTTTCTTTATTTATTTCTGTGA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATTGCTATAATGGTGAAGTTAATTTCCAAAGGAAAAATGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysIleTrpPheAlaLysGlu--- 714
QY 2232 TCAAGCATGAGCACTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726
RESULT 15
ID ABO34295
XX ABO34295 standard; protein; 787 AA.
AC ABO34295;
XX
DT 19-SEP-2003 (first entry)

XX Human secreted/transmembrane polypeptide PRO 21340.
DE Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.
XX
OS Homo sapiens.
XX US2003044934-A1.
XX 06-MAR-2003.
XX 28-AUG-2002; 2002US-00230338.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-492274/46.
XX N-PSDB; ACD82220.
XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes.
XX Claim 19; Fig 90; 315pp; English.
XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. Nucleic acids that encode PRO can be used to generate either
XX transgenic animals or knock-out animals useful in developing and
XX screening of therapeutically useful reagents. The nucleic acids may also
XX be used in gene therapy for replacing defective gene, in chromosome
XX identification, as chromosome markers, or in generating probes to isolate
XX full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
XX stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
XX and for detecting the presence of tumour in an animal. The PRO
XX polypeptides are useful as molecular markers for protein electrophoresis
XX and the isolated nucleic acids may be used for recombinantly expressing
XX those markers. The PRO polypeptides and nucleic acids may also be used in
XX tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
XX PRO and in affinity purification of PRO from recombinant cell culture or
XX natural sources. The present sequence represents the amino acid sequence
XX of a human secreted/transmembrane PRO polypeptide
SQ Sequence 787 AA;
Alignment Scores:
Pred. No.: 3,08e-127 Length: 787
Score: 1524.50 Matches: 310
Percent Similarity: 58.89% Conservative: 134
Best Local Similarity: 41.11% Mismatches: 259
Query Match: 31.79% Indels: 51
DB: 6 Gaps: 18
US-10-054-683-18 (1-2640) x ABO34295 (1-787)
QY 72 ATGTGGTCTTCTTCTCTCAGCGGCTCGCGGGCTCGCGATGAC---AGTAATTTT 128
Db 4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21.
QY 129 GATAGTTTACCTGTCACAAATTACAGTTCCGGAGAAATACGGTCAATTAAGAAGGA 188
Db 22 GlnAsnSerLeuLeuGlnIleValIleProGluLysIleGlnThrAsnThrAsnAspSer 41
QY 189 ATTGAA-----TCGAGGCATCTCCACAAATTTGTAATTAAGAGGAACCATATACT 239
Db 42 SerGluIleGluTyrGluGlnIleSerTyrIleIleProfileAspGluLysLeuTyrThr 61

Qy	240	GTGAATTTAATGCAAAAAA	CTTTTATCCCAATATTTT	TAGAGTTTACAGTTATAGTGGC	299
Db	62	ValHisLeuLysGlnA-rGtyrPheLeuAlaAspAsn	PheMetIleTyrLeuTyrAsn---	80	
Qy	300	ACAGAAATTTATGAACAC	CTTGACCAAGATTTTCAGA	ATTTCTGCCTACTACCAAGGGTAT	359
Db	81	GlnGlySerMetAsnThrTyrSerSerAsp	legInThrGlnCysTyrTyrGlnGlyAsn	100	
Qy	360	ATTGAAGGTTATCCAAAT	CTGTGGTGATGGTTAGC	ATGATCTGACTCAGCGGGCGTA	419
Db	101	IleGluGlyTyrProAspSerMetValThrLeuSer	ThrCysSerGlyLeuAsgGlyIle	120	
Qy	420	CTACAGTTTGAATGTTAGT	TATGGAAATAGAACCCCT	GAGTCTTCAGTTGGCTTTGAA	479
Db	121	LeuGlnPheGluAsnValSerTyrGlyIleGlu	ProLeuGluSerAlaValGluPheGln	140	
Qy	480	CATGTAATTTACCAAGTAA	ACATACAGAAAGCAGATG	TTTCTTTATATATAGAGAGGAT	539
Db	141	HisValLeuTyrLysLeuLysAsnGluAspAsn	AspIleAlaPheIleAspArgSer	160	
Qy	540	ATTGAATCAAGA-----	GATCTGTCCTTTAAATTA	CAAAAGCCGACGAGCCACAGCAA	590
Db	161	LeuLysGluGlnProMetAspAspAsnIle	PheIleSerGluLysSerGluProAlaVal	180	
Qy	591	GAT-----TTTGCAAGT	TATAGAAATGCAATGAT	TCTTATAGTTGAAAACAATTTGATAAT	644
Db	181	ProAspLeuPheProLeuTyrLeuGlu	MetHisIleValValAspLysThrLeuTyrAsp	200	
Qy	645	CATATGGGGTCTGATACA	CACTTGTCGCTCAAAAGT	TTTTTCCAGTTGATGGATTCAGC	704
Db	201	TyrTrpGlySerAspSerMetIleValThr	AsnLysValIleGluIleValGlyLeuAla	220	
Qy	705	AATGCTATTTTGTTCATTA	TATATTAATTAATTCAT	TCTGCTTCATTTGGAGCTTTGGATA	764
Db	221	AsnSerMetPheThrGlnPheLysValThrIle	ValLeuSerSerLeuGluLeuTrpSer	240	
Qy	765	GATGAAATATAAATTTGCA	CCACCTGGAGAGCTAAT	CAGTATTATACACATTTTTTAAGA	824
Db	241	AspGluAsnLysIleSerThrValGlyGluAla	AspGluLeuLeuGlnLysPheLeuGlu	260	
Qy	825	TGGAACAATCTTATCTTT	TGTTTACGTGCTCATGAT	GTGGCATTTTTTACTTGTGTTACAGA	884
Db	261	TrpLysGlnSerTyrLeuAsnLeuArgPro	HisAspIleAlaTyrLeuLeuIleTyrMet	280	
Qy	885	GAAAGTCAAAATATATG	TGTGGTGCACCTTTCA	AGGGAAGATGTGTAGTCAAACTATGCA	944
Db	281	AspTyrProArgTyrLeuGlyAlaValPhe	ProGlyThrMetCysIleThrArgTyrSer	300	
Qy	945	GGAGGTGTTGTTCTGCA	CCCCCAGAACCATAGCT	TGGAATCACTTGCCAGTATTTTAGCT	1004
Db	301	AlaGlyValAlaLeuTyrProLysGluIle	ThrLeuGluAlaPheAlaValIleValThr	320	
Qy	1005	CAATTATTTAGCCCTTAG	TATGGGATCACCTTATG	ATCATGACATTAACAAATGCCAGTGTCTCA	1064
Db	321	GlnMetLeuAlaLeuSerLeuGlyIle	SerTyrAspAspProLysLysCysGlnCysSer	340	
Qy	1065	GGAGCTGCTGCANTATT	GAATCCAGAAGCAATTC	ATTTCATTTAGTGGTGTGAAGATCTTTAGT	1124
Db	341	GluSerThrCysIleMetAsn	ProGluValValGlnSerAsnGlyValLysThrPheSer	360	
Qy	1125	AATCGCAGCTTCGAAG	ACTTTGCACTTTTATTT	CAAGCAGAAGTCCCAGTGTCTTCAC	1184
Db	361	SerCysSerLeuArgSerPhe	GlnAsnPheIleSerAsnValGlyValLysCysLeuGln	380	
Qy	1185	AATCAGCTCTCGTCTAG	ATCTCTTTTCAACAGCA	GCAGCTGTGTGTTAATGCAAAAGCTG	1244
Db	381	AsnLysProGlnMetGln	Lys---LysSerProLysProValCysGlyAsnGlyArgLeu	399	
Qy	1245	GAACGACGAGAGGATGT	GTACTGTGGAGCTGAAC	AGGATTTGTCCTTATTTGGAGAAACA	1304
Db	400	GluGlyAsnGluIleCysAsp	CysGlyThrGluAlaGlnCysGly-----ProAlaSer	417	

Search completed: January 10, 2005, 21:47:45
Job time : 397.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 10, 2005, 21:32:40 ; Search time 90.5 Seconds

(without alignments)
5613.530 Million cell updates/sec

Title: US-10-054-683-18

Perfect score: 4796

Sequence: 1 catctgcacttccaaactgc.....actgttacatttcaaaaaa 2640

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=cpn2 1/USPTO spool_p/US10054683/runat 10012005 174510 15504/app query.fasta 1.2823
-DB=PIR75 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10054683 @CGN 1 1 135 @runat 10012005 174510 15504 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3984	83.1	734	JC4861	fertilin beta cha
2	3687.5	76.9	735	G02937	fertilin beta - cr
3	1384.5	28.9	756	S47656	tMDC II protein -
4	1365.5	28.5	736	S47645	tMDC I protein - c
5	1292	26.9	823	S18968	cytostatin precurs
6	1288	26.9	777	I48100	ADAM 5 protein pre
7	1186	24.3	357	S23403	sperm surface prot
8	1101	23.0	655	JC7850	disintegrin and me
9	1033.5	21.5	825	S55060	fertilin alpha-II
10	1022.5	21.3	905	S55059	fertilin alpha-I -
11	1016.5	21.2	660	S71949	metalloproteinase
12	857	17.9	903	S60257	metrin alpha - mo
13	795	16.6	600	I49281	fertilin alpha pre
14	766	16.0	836	A60385	monocyte surface a

15	762	15.9	609	2	S55270	catrocollastatin p
16	732	15.3	732	2	I52361	testicular metallo
17	729	15.2	732	2	S48160	metalloproteinase
18	723	15.1	814	2	G02390	disintegrin-like m
19	719.5	15.0	571	2	S24789	jararhagin C precu
20	712.5	14.9	735	2	I48101	ADAM 6 protein pre
21	710.5	14.8	616	2	A55796	ecarin precursor -
22	699	14.6	776	2	S28258	androgen-regulated
23	696.5	14.5	789	2	S28259	androgen-regulated
24	695	14.5	670	2	I65967	disintegrin-like m
25	692.5	14.4	713	2	I65253	disintegrin-like t
26	663	13.8	610	2	JC7530	vascular apoptosis
27	653.5	13.6	610	2	JC8056	halyasease - Glydiu
28	641	13.4	952	2	T18900	disintegrin and me
29	616.5	12.9	429	2	A42972	coagulation factor
30	614.5	12.8	416	2	A37877	hemorrhagic protei
31	606	12.6	419	2	S41607	atrolysin A (EC 3.
32	594.5	12.4	419	2	A59414	metalloproteinase
33	584.5	12.2	549	2	S48169	metalloproteinase
34	568	11.8	473	2	I49283	ADAM 4 protein pre
35	561.5	11.7	524	2	S38539	disintegrin-like m
36	553	11.5	478	2	A43296	atrolysin E (EC 3.
37	535	11.2	484	2	JC8020	metalloproteinase-
38	533	11.1	480	1	A30065	trigramin precurs
39	530.5	11.1	481	2	JC4342	fibrinolytic prote
40	530.5	11.1	481	2	S43125	trigramin precursor
41	501	10.4	478	2	JQ1301	hemorrhagic protei
42	486.5	10.1	1042	2	T26644	hypothetical prote
43	467	9.7	478	2	JC4880	fibrinolytic metal
44	393.5	8.2	414	2	S41608	atrolysin B (EC 3.
45	392.5	8.2	411	1	HYSNFA	fibrolase (EC 3.4.

ALIGNMENTS

RESULT 1

JC4861
fertilin beta chain - human
C:Species: Homo sapiens (man)
C>Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4861
R:Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A:Title: Molecular cloning of the human fertilin beta subunit.
A:Reference number: JC4861; MUID:96295488; PMID:8702389
A:Accession: JC4861
A:Molecule type: mRNA
A:Residues: 1-734 <CUP>
A:Cross-references: UNIPROT:Q99965; GB:U38805; NID:G4151118; PIDN:AD04206.1; PID:G415111
C:Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: glycoprotein; integrin binding; transmembrane protein
F:382-734/Product: fertilin beta chain #status predicted <NAT>
F:382-467/Domain: disintegrin homology <DIS>
F:448-450/Region: integrin binding #status predicted
F:686-708/Domain: transmembrane #status predicted <TMW>
F:121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:			
Pred. No.:	1.32e-286	Length:	734
Score:	3984.00	Matches:	734
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	83.07%	Indels:	0
DB:	2	Gaps:	0

US-10-054-683-18 (1-2640) x JC4861 (1-734)

QY	72	ATGTGGTCTTGTTCCTCAGCGGCTCGCGGCTCGGATGACAGTAATTTTGT	131
Db	1	MetTrpValLeuPheLeuLeuSerGlyLeuGlyLeuArgMetAspSerAnPheAap	20
QY	132	AGTTTACCTGTGCAATTACGTTCCGAGAAAATACGTCATATAATAAGGAAGNAAT	191

Db	21	SerLeuProValGlnIleThrValProGluLysIleArgSerIleIleLysGluGlyIle	40
QY	192	GAATCCGAGCATCTTACAAAATTGTAATTGAAGGGAACCATATATCTGTGAATTTAATG	251
Db	41	GluSerGlnAlaSerTyrLysIleValIleGluGlyLysProTyrThrValAsnLeuMet	60
QY	252	CAAAAAACCTTTTACCCCATAAATTTAGAGTTTACAGTTATAGTGGCAGAGAAATTATG	311
Db	61	GlnLysAsnPheLeuProHisAsnPheArgValTyrSerTyrSerGlyThrGlyIleMet	80
QY	312	AAACCACTTGACCAAGATTTTCAGAAATCTCCACTACCAAGGTATATTGAAGTTAT	371
Db	81	LysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGlyTyr	100
QY	372	CCAAAATCTGTGTGTGGTTAGCATGTACTGTGAGCTCAGGGCGCTACTACAGTTTGAA	431
Db	101	ProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGlu	120
QY	432	AATGTTAGTTATGGAATAGAACCCCTGGAGTCTTTCAGTTGGCTTTCAGACATGTAATTAC	491
Db	121	AsnValSerTyrGlyIleGluProLeuGluSerSerValGlyPheGluHisValIleTyr	140
QY	492	CAAGTAAACATAGAAGCAGATGTTTCTTATATATGAGAGGATATTTGAATCAAGA	551
Db	141	GlnValLysHisLysLysAlaAspValSerLeuTyrAsnGlnLysAspIleGluSerArg	160
QY	552	GATCTGTCTTTAAATTTACAAAGCGCAGAGCCACAGCAAGATTTGCAAGTATATAGAA	611
Db	161	AspLeuSerPheLysLeuGlnSerAlaGluProGlnAspPheAlaLysTyrIleGlu	180
QY	612	ATGCATGTTATAGTTGAAAACAAATGTTATATCAATATGGGCTCGATACAACTGTGTC	671
Db	181	MetHisValIleValGluLysGlnLeuTyrAsnHisMetGlySerAspThrValVal	200
QY	672	GCTCAAAAGTTTCCAGTTGATTGGATTGACGAATGCTATTGTTTGTCTATTATTAATT	731
Db	201	AlaGlnLysValPheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAsnIle	220
QY	732	ACAAATTTCTGCTCTTCATTTGGAGCTTTGGATAGATGAAATAAATTTGCAACACTGGA	791
Db	221	ThrIleIleLeuSerSerLeuGluLeuTyrIleAspGluAsnLysIleAlaThrThrGly	240
QY	792	GAACCTAATGCTTTATACACACATTTTAAAGTGGAAACATCTTATCTGTTTACGT	851
Db	241	GluAlaAsnGluLeuLeuHisThrPheLeuArgTyrLysThrSerTyrLeuValLeuArg	260
QY	852	CCTCATGATGTGGCATTTTACTTTGTACAGAGAAAGTCAAAATATGTTGGTGCAACC	911
Db	261	ProHisAspValAlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAlaThr	280
QY	912	TTTCAAGGAAGATGTGTGATGCAAACTATCCAGAGGTGTGTTCTGCACCCAGAAC	971
Db	281	PheGlnGlyLysMetCysAspAlaAsnTyrAlaGlyGlyValValLeuHisProArgThr	300
QY	972	ATAAGTCTGGAATCACITGCGATTTTACTCAATTTAGCTTACCTTAGTATGGGATC	1031
Db	301	IleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyIle	320
QY	1032	ACTTATGATGATTAACAAATGCGAGTGCTCAGAGCTGTCTGCATTTATGAATCCAGAA	1091
Db	321	ThrTyrAspAspIleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnProGlu	340
QY	1092	GCAATTCATTTTCAGTGGTGAAGATCTTTAGTAACCTACGCTTCGAGCTTTCGACAT	1151
Db	341	AlaIleHisPheSerGlyValLysIlePheSerAsnCysSerPheGluAspPheAlaHis	360
QY	1152	TTTATTTCAAGCAGAGTCCAGGTCTTCACATCAGCTCGCTAGATCTCTTTTTC	1211
Db	361	PheIleSerLysGlnLysSerGlnCysLeuHisLeuGlnProArgLeuAspPhePhe	380
QY	1212	AAACAGCAGCAGTGTGTGGTAAATCCAAAGCTGGAAAGCAGAGAGATGTGACTGTGGG	1271
Db	381	LysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluGluCysAspCysGly	400
QY	1272	ACTGACAGGATTTGGCCCTTATTGGAGAAACATGCTGTGATATTTGCCACATGTAGATT	1331
Db	401	ThrGluGlnAspCysAlaLeuIleGlyGluThrCysCysAspIleAlaThrCysArgPhe	420
QY	1332	AAAGCCGGTTCAAACTGTCTGTAAGGACCATGCTCGCAAAACTGTCTATTTATGTCAAAA	1391
Db	421	LysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSerLys	440
QY	1392	GAAAGAAATGTGTAGCCCTTCTTGAAGAAATGCGACCTCCCTCGAATATATGCAATGATCA	1451
Db	441	GluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGlySer	460
QY	1452	TCGTGATCTGATGAGTGGAGTTTGTATGAGTGGGATAAACAATGTATACACACATTTGGC	1511
Db	461	SerAlaSerCysProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsnGln	480
QY	1512	TGGATCTGTATAGATGGAGTTTGTATGAGTGGGATAAACAATGTATACACACATTTGGC	1571
Db	481	TrpIleCysIleAspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPheGly	500
QY	1572	AAAGAAATGATGTTGGCCCTTCAGAAATGTTATTTCTCACCTTAATTCAGAGCTGATGA	1631
Db	501	LysGluValGluPheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAspVal	520
QY	1632	TCGTGAAACTGTGGTATAGTATTGAGTATACACAGTGTGAAGCTGACAACTCTGCAG	1691
Db	521	SerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeuGln	540
QY	1692	TGCGGAAATTAATATGTAATATATGTAATAATTTTATTAACAATTTCCAAGAGCCACT	1751
Db	541	CysGlyLysLeuIleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAlaThr	560
QY	1752	ATTATTTATGCCAACATAAGTCGACATCTCTCATTTGCTGTGGAATTTGCCAGTGCATAT	1811
Db	561	IleIleTyrAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAspHis	580
QY	1812	GCAGACAGCAAAAGATGTGGATAAAGATGAAACTTCTTGTGGTTCAAAATGAAGTTTC	1871
Db	581	AlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysValCys	600
QY	1872	AGGAATCAAAAGATGTGTGAGTCTTCATCTTGGGGTTATGATTTACTACTGACAAATGC	1931
Db	601	ArgAsnGlnArgCysValSerSerTyrLeuGlyTyrAspCysThrThrAspLysCys	620
QY	1932	AATGATAGAGGTGTATGCAATAACAAAGACACTGTCACTGTAGTGTCTTCAATTTACCT	1991
Db	621	AsnAspArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeuPro	640
QY	1992	CCAGATTGCTCAGTTCATCAATCAGATCTATGCGCTGGTGGAGTATTCACAGTGGCAATTTT	2051
Db	641	ProAspCysSerValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAsnPhe	660
QY	2052	CCAACCTGTAGCTATACAGCCAGACTCCCTGAAAGCGGTACATTCAGAGACATTTACCAT	2111
Db	661	ProProValAlaIleProAlaArgLeuProGluArgTyrIleGluAsnIleTyrHis	680
QY	2112	TCCAAACCAATGAGATGGCCATTTTCTTATTTCTTCTTCTTCTTCTTCTTCTTCTGTA	2171
Db	681	SerLysProMetArgTyrProPhePheLeuPheIleProPhePheIleIlePheCysVal	700
QY	2172	CTGATTTGCTATAATGGTGAAGTTAATTTCCAAAGGAAAAATGGAGAACTGAGGACTAT	2231
Db	701	LeuIleAlaIleMetValLysValAsnPheGlnArgLysLysTyrArgThrGluAspTyr	720
QY	2232	TCAGCGATGAGCAACCTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	2293
Db	721	SerSerAspGluGlnProGluSerGluSerGluProLysGly	734
RESULT 2			
G02937			
fertilin beta - crab-eating macaque			

C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02937; S55061
R;Ramatoao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
submitted to the EMBL Data Library, August 1995
A;Reference number: G12615
A;Accession: G02937
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-735 <RAM>
A;Cross-references: UNIPROT:Q28478; EMBL:U33959; NID:g998339; PID:g998340
R;Perry, A.C.P.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A;Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A;Reference number: S55059; MUID:95260313; PMID:7741716
A;Accession: S55061
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-722, 'S', 724-735 <PER>
A;Cross-references: EMBL:X77653; NID:g794076; PIDN:CAA54733.1; PID:g794077
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;383-468/Domain: disintegrin homology <DIS>

Alignment Scores:

Pred. No.:	1.le-264	Length:	735
Score:	3687.50	Matches:	671
Percent Similarity:	95.51%	Conservative:	31
Best Local Similarity:	91.29%	Mismatches:	32
Query Match:	76.89%	Indels:	1
DB:	2	Gaps:	1

US-10-054-683-18 (1-2640) x G02937 (1-735)

Qy	72	ATGTGG---GTCTGTTTCTGCTCAGCGGGCTCGGGGCTCGGATGGACGTAATTTT	128
Db	1	MetTrrpValValluPheLeuLeuSerGlyLeuGlyLeuTrpMetAspSerAsn	20
Qy	129	GATGATTTTACCTGTGCAAAATTACAGTTCCGGAGAAAATACGGTCAATAATAAAGGAAGGA	188
Db	21	AspSerLeuProValGlnIleThrValProGluLysIleArgSerIleIleLysGlu	40
Qy	189	ATTGAATCGGAGGATCCTACAAATGTAAATGTAATGAAGGGAACCATATATCTGTAATTA	248
Db	41	IleGluSerGlnValSerTyrLysIleValIleGluGlyLysProTyrThrAlaAsnLeu	60
Qy	249	ATGCAAAAACCTTTTACCCCATATTTTAGAGTTTACAGTTTATAGTGGCACAGGAAT	308
Db	61	MetGlnLysAsnPheLeuSerHisAsnPheArgValTyrSerTyrAsnGlyThrGlyIle	80
Qy	309	ATGAAACCACTTGACCAAGATTTTCAGAAATTTCTGCCACTACCAAGGGTATATTGAAGGT	368
Db	81	MetLysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGly	100
Qy	369	TATCCAAATCTGTGTGATGGTTAGCACATGTACTGGACTACGGGCGTACTACAGTTT	428
Db	101	TyrProLysSerValAlaMetValSerThrCysThrGlyLeuArgGlyLeuLeuGlnPhe	120
Qy	429	GAAAATGTTAGTTATGAATAGAACCCCTCGAGTCTTCAGTTCGCTTGAACATGTAATT	488
Db	121	GluAsnValSerTyrGlyIleGluProLeuGluSerValGlyPheGluHisValIle	140
Qy	489	TACCAAGTAAACATAAGAAGCAGATGTTTCCCTTATATATGAAGGATATTGAATCA	548
Db	141	TyrGlnValLysHisLysLysAlaAspValSerLeuTyrAsnGluLysAspIleGluSer	160
Qy	549	AGAGATCTGCTTTAAATTAACAAAGCGCAGAGCCACAGCAAGATTTTGCAAAGTATATA	608
Db	161	ArgAspLeuSerPheLysLeuGlnSerIleGluProGlnLysAspPheAlaLysTyrIle	180
Qy	609	GAAATGATCTTAGTTGAAAACCAATTCATATCATATGGGTCTGTATACACTGTT	668
Db	181	GluMetHisValValGluLysGlnLeuTyrAsnHisMetGlySerGlyThrVal	200

Qy	669	GTGCTCTCAAAAGAGTTTCCAGTTTGATGGATTGCAAGATCTATTTTGTTCATTAAT	728
Db	201	ValThrGlnLysIlePheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerLeuAsn	220
Qy	729	ATTACAAATATTCTGCTCTTCATTGGAGCTTTGGATAGATGAAATATAAATTTGCAACACT	788
Db	221	IleThrValIleLeuSerSerLeuGluLeuTrpIleAspGluAsnLysIleAlaThrThr	240
Qy	789	GGAGAAGTAATCAGTTATTACACACATTTTAAAGATGGAAAAACATCTTATCTTGTTTA	848
Db	241	GlyAspAlaLysGluLeuLeuHisThrPheLeuArgTrpLysArgSerTyrLeuValLeu	260
Qy	849	CGTCTCTATGATGTGGCATTTTACTTTGTTCACAGAAAAGTCAATATATGTTGGTCA	908
Db	261	ArgProHisAspValAlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAla	280
Qy	909	ACCTTTCAAGGGAAGATGTGTGATGCAAACTATGCAGGAGGTCTGTCTGCACCCCGAGA	968
Db	281	ThrPheGlnGlyLysMetCysAspAlaAsnTyrAlaGlyValLeuLeuHisProArg	300
Qy	969	ACCATAAGTCTGGAATCAGTTGAGCTTATTTTATAGCTCAATTTATGAGCCTTAGTATGGG	1028
Db	301	ThrIleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGly	320
Qy	1029	ATCATTTATGATGACATTAACAATGCCAGTGTCTCAGGAGCTGTCTGCATTTATGAATCCA	1088
Db	321	IleProTyrAspAspIleAsnGlnCysGlnCysSerAlaAlaValCysIleMetAsnPro	340
Qy	1089	GAGCAATTCATTTAGTGTGTGAAGATCTTTAGTAACATGCAGCTTCGAGAGCTTTGCA	1148
Db	341	GluAlaIleHisPheSerGlyValLysIlePheSerAsnCysSerIleGluAspPheAla	360
Qy	1149	CATTTTATTTCAAGCAGAGTCCCAAGTGTCTTCACAATCAGCTCGCTTAGATTCCTTTT	1208
Db	361	HisPheIleSerLysGlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPhe	380
Qy	1209	TTCAAAACAGACAGTGTGTGTAATGCAAAGCTGGAAGCAGAGAGAGTGTGACTGT	1268
Db	381	PheLysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluCysAspCys	400
Qy	1269	GGACCTGACACAGATTTGTCCTTATTGGAAGAACATGCTGTGATATTGCCACATGAGA	1328
Db	401	GlyThrGlnGlnAsnCysPheLeuLeuGlyAlaLysCysAspThrAlaThrCysArg	420
Qy	1329	TTTAAAGCCGGTTTCAAACTGTCTGAAGGACCACTGTGCGAAAACCTGTCTTATTATGCA	1388
Db	421	PheLysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSer	440
Qy	1389	AAAGAAGAAATGTGTAGGCTTCTTTGAAGAAATGCGACCTCCCTCGAATATTGCAATGGA	1448
Db	441	GlnGluArgValCysArgProSerPheAspGluCysAspLeuProGluTyrCysAsnGly	460
Qy	1449	TCATCTGCATCATGCCAGAAAACCACTATGTTTCAGACTGGGCATCGTGTGACTCAAT	1508
Db	461	ThrSerAlaSerCysProGluAsnHisPheIleGlnThrGlyHisProCysGlyProAsn	480
Qy	1509	CAATGATCTGTATAGATGGAGTTTCTATGAGTGGGATAAACAATGTACAGACACATTT	1568
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Qy	1569	GGCAAAAGATAGAGTTTGGCCCTTCAAGATGTTTATCTCACCTTAAATTCAAAGACTGAT	1628
Db	501	GlyGlyGluAlaGluPheGlyProThrGluCysTyrSerTyrLeuAsnSerLysThrAsp	520
Qy	1629	GTATCTGGAACCTGCTGATAGTATCAGGATACACAGTGTGAAGCTGCAATCTG	1688
Db	521	ValSerGlyAsnCysGlyIleGlyAspSerGlyTyrThrGlnCysGluAlaAspAsnLeu	540
Qy	1689	CAGTGGGAAAAATTAATATGTAATATGATAGTAAATTTTATTACAAATTTCAAGAGCC	1748
Db	541	GlnCysGlyLysLeuIleCysLysTyrAlaGlyPheLeuLeuGlnIleProArgAla	560
Qy	1749	ACTATTATTATGCCAACATAAGTGGACATCTCTGCATTCGTGGAAATTTGCGAGTGAT	1808

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Db 561 ThrIleIleTyrAlaAsnIleSerGlyHisLeuCysValAlaValGluPheAlaSerAsp 580
Qy 1809 CATCAGACGACCAAGATGCTGATAAAGATGGAACCTCTTCTGCTTCAATAAGGTT 1868
Db 581 HisGluAspSerHisLeuMetTrpIleLysAspGlyThrSerCysGlySerAsnLysVal 600
Qy 1869 TGCAGGAATCAAGATGTGTAGTCTTCTCATCTTGGCTGTATGATGTTACTTACACAAA 1928
Db 601 CysLysAsnGlnArgCysValSerSerTyrLeuGlyTyrAspCysThrAspLys 620
Qy 1929 TGCATGATGAGTGTATGCAATAACAAAAGACATGCTCACTGTAGTCTTCAATTTA 1988
Db 621 CysAsnHisArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeu 640
Qy 1989 CTTCCAGATTCTCAGTTCATCATGATCTATGGCTGTGGTGGATATTGACAGTGGCAAT 2048
Db 641 ProProAspCysSerValGlnSerAspThrSerProGlyGlySerIleAspSerGlyAsn 660
Qy 2049 TTTCACCTGTAGCTATACACGACGAGCTCCCTCAAGGCGCTACATTTGAAACATTTAC 2108
Db 661 PheProLeuValAlaValProAlaArgLeuProGluArgArgHisMetGluAsnValTyr 680
Qy 2109 CATTCAAAACAAATGAGATGGCCATTTCTTATTATTCTTCTTCTTATTATTCTGT 2168
Db 681 HisSerLysProMetArgTrpProLeuPheLeuPheIleProPhePheIlePheCys 700
Qy 2169 GTACTGATCTCTAATGTTGAAGTTAATTTCCAAAGGAAATCGAGAACTGAGGAC 2228
Db 701 ValLeuIleAlaIleMetValLysValHisPheGlnArgLysIleTrpArgThrGluAsp 720
Qy 2229 TATTCAAGCGATGAGCAACTGAAAGTGAGAGTGAGAGTCAACTAAAGG 2273
Db 721 TyrSerThrAspGluGlnProGluSerGluSerGluProLysGly 735

RESULT 3
S47656
tMDC II protein - crab-eating macaque
C/Species: Macaca fascicularis (Crab-eating macaque)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S47656
R/Perry, A.C.F.; Barker, H.L.; Jones, R.; Hall, L.
Biochim. Biophys. Acta 1207, 134-137, 1994
A/Title: Genetic evidence for an additional member of the metalloproteinase-like, disint
C/Reference number: S47656; MUID:94318664; PMID:8043604
A/Accession: S47656
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-756 <PER>
C/Cross-references: UNIPROT:Q28483; EMBL:X77619; NID:9531477; PIDN:CAA54713.1; PID:95314
C/Superfamily: mouse meltrin alpha; disintegrin homology
P/388-473/Domain: disintegrin homology <DIS>

Alignment Scores:
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Score: 1384.50 Matches: 296
Percent Similarity: 53.85% Conservative: 124
Best Local Similarity: 37.95% Mismatches: 294
Query Match: 28.87% Indels: 66
DB: 2 Gaps: 18

US-10-054-683-18 (1-2640) x S47656 (1-756)
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Qy 138 CCTGTGCAAAATTACAGTTCGGGAGAAATACGGTCAATA---ATAAAGGAAGCAATTGAA 194
Db 24 PheLeuGlnThrIleProGluLysIleSerSerAspAlaLysThrAspProGlu 43
Qy 195 TCGCAGGCATCCTACAAAATTGTAATTTGAAGGAAACCATATACTGTGAATTTAATGCA 254
Db 195 TCGCAGGCATCCTACAAAATTGTAATTTGAAGGAAACCATATACTGTGAATTTAATGCA 254
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Db 64 GlnSerIleLeuSerSerAlaSerPheIleHisSerTyrAspLysAsnAspIleArgHis 83
Qy 309 ATGAAAACCATCTTACCAAGATTTTTCAGAAATTTCTGCCACCTACCAAGGATATATTGAAGGT 368
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Db 102 IleProAsnSerLeuValThrLeuSerValCysSerGlyLeuArgGlyThrMetGlnLeu 121
Qy 429 GAAAATGTTAGTTATGATAGTAAACCCCTGGAGTCTTCACTTGGCTTTGAACATGTAATT 488
Db 122 LysAsnIleSerTyrGlyIleGluProMetGluAlaValSerGlyPheIleHisLysIle 141
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Db 142 TyrGluGluLysPheAlaAspThrAsnIleLeuLeuGluAlaAsnAspThrTyrSerTyr 161
Qy 549 AGAGATCTGTCTTAAATTAACAAAGCGCAGACGACCAAGCAAGATTTTGCAGAG----- 602
Db 162 PheAsnSerGluTyrGlnValArgLysSerSerGluLysThrAspPheIleLysLeuPhe 181
Qy 603 -----TATATAGAAATGCAATGTTATAGTTGAAACAAATGTTATATATATATATATAT 656
Db 182 ProArgTyrIleGluMetHisIleValAlaAspLysAsnLeuPheAspTyrMetGlySer 201
Qy 657 GATACAACTGTTGCTGCTCAAAAGTTTTCCAGTTGATTTGATTTGATTTGATTTGATTTT 716
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Qy 717 GTTTCATTAATATATCAATTTCTGCTCTTCAATTTGAGCTTTGGATAGATGAAATATAA 776
Db 222 ThrGlnLeuGlnLeuThrValIleIleSerSerIleGluIleTrpSerAsnLysAsnLys 241
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Qy 837 TATCTGTTTGTAGTCTCTCATGATGGCAATTTTACTTTTACAGAGAAAGTCAAAAT 896
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Qy 897 TATGTTGTCACCTTTCAAGGAAGATGTGTGATGCAAACTATCGCAGGAGGTGTGTT 956
Db 282 LeuIleGlyAlaThrPheProGlyGlnValCysAsnLysAspPheAlaAlaValAla 301
Qy 957 CTGACCCCAAGAACCATAGTCTGGAATCACTTGGAGTTATTTAGTCAATTTATTTAGC 1016
Db 302 LeuTyrProGluGlyLeuSerLeuGluSerTyrThrValIleIleValGlnLeuLeuGly 321
Qy 1017 CTTAGTATGGGATCACTTATGATGACATTAACAAATGCGCAGTGTCTCAGAGCTGTCTGC 1076
Db 322 LeuAsnLeuGlyLeuThrTyrAspLysThrAspThrCysHisCysSerGlyAspValCys 341
Qy 1077 ATTATGAATCCAGAAGCAATTCATTTCTGCTGTGAGATCTTTAGTAAGTCTGAGTTC 1136
Db 342 ThrMetThrProLysAlaValTyrSerGlyValLysAspPheSerValCysSerLeu 361
Qy 1137 GAAGACTTTGCACATTTTATTTTCAAGAGCAGAAAGTCCAGTGTCTTACAAATCAGCTCGC 1196
Db 362 AspAspPheLysTyrIleSerSerHisAsnGlyLeuThrCysLeuGlnThrAsnProLeu 381
Qy 1197 TTAGATCTCTTTTCAACAGCAGCAGTGTGTGTGTAATGCAAGCTGGAAGCAGGAGAG 1256
Db 382 GluMetProThrTyrThrGlnArgArgIleCysGlyAsnGlyLeuLeuGluGlyGlyGlu 401
Qy 1257 GAGTGTGCTGTGGACTGAACAGGATTTGTCCTTATTGGAGAAACATCTGTGTATTT 1316
Db 402 GluCysAspCysGlyAsnLysAspAsnCysThr-----HisLysLeuCysCysAspAla 419
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Db      212  GluLysValPheGlnIlePheGlyLeuIleAenThrMetPheSerGlnLeuAenIleThr 231
QY      735  ATTATTCCTCTTCATTCAGGCTTTGGATAGTAAATATAAATGCAACACTGGAGAA 794
Db      232  ValMetLeuSerSerLeuGluIleThrPheSerGlnAenIleSerThrSerGlyHis 251
QY      795  GCTAATAGTATTATACACACATTTTAAAGATGGAACATCTTATCTCTGTTTACGTCCT 854
Db      252  AlaAspGluIleLeuGlnArgPheLeuLeuThrPheGlnLysLeuLeuPheGlnArgSer 271
QY      855  CATGATGGCAATTTTACTGTTTACAGAGAAAGTCAAAATATGTTGGTGCACACTTT 914
Db      272  HisAspMetThrThrLeuLeuIleThrArgAenHisSerThrThrValGlyAlaThrThr 291
QY      915  CAAGCGAAGATGTGTGATGCAAACTATCGACGAGGTGTGTTCTGCACCCCGACAGACATA 974
Db      292  HisGlyMetAlaCysAspProLysPheAlaThrGlyIleAlaLeuThrProLysIle 311
QY      975  AGTCTGGAATCACTTGCAGTTTATTTAGCTCAATATTAGCCTTAGTATGGGATCACT 1034
Db      312  ThrValGluAlaPheSerValValMetAlaGlnLeuLeuGlyIleAenLeuGlyLeuThr 331
QY      1035  TATGATGACATTAAACAATGCGAGTCTCAGAGCTGTCTGCATATGATTCAGAGACA 1094
Db      332  TyrAspAspIleThrAsnCysThrCysProGlyProThrCysIleMetAsnProAspAla 351
QY      1095  ATTCAATTCAGTGTGTGAAGATCTTTAGTAACAGCTTCGAGCTTCGAGACTTTGGACATTT 1154
Db      352  IleArgSerHisGlyMetLysPhePheSerSerCysSerMetAspGluPheLysGlnIle 371
QY      1155  ATTTCAAAGCAAGATCCCAGTGTCTTCACAATCAGCCTCGCTTAGATCTCTTTTCAAA 1214
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QY      1215  CAGCAACAGTGTGTGTAATGCAAGCTGGAACGAGAGAGTGTGACTGTGGACT 1274
Db      392  LysSerAlaThrCysGlyAsnGlyIleLeuGluProThrGluGlnCysAspCysGlyTyr 411
QY      1275  GAACGAGTGTGCTCCCTTATTGGAGAAACATGCTGTGTATATTGCCACATGTAGATTAAA 1334
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QY      1335  GCCGGTTCAAACCTGTGCTGAAGACCATGCTGCGAAAC-----TGCTATTATTATGCTA 1388
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QY      1449  TCATCTGCATCATGCCAGAAACCACTATGTTTCAGACTGGGCATCGCTGGACTGAAT 1508
Db      470  ThrSerGluPheCysValProAspValLysAlaAlaAspLeuGluTyrCysSerAsnLys 489
QY      1509  CAATGGATCTGTATAGATGAGTTTGTATGAGTGGGATAAACAATGATACAGACACATTT 1568
Db      490  ThrSerTyrCysPheLysGlyIleCysArgAspArgAspArgGlnCysSerGlnLeuPhe 509
QY      1569  GGCAAAAGATAGATTGTCCTTCAGAAATGTTATCTCACCTTAATTCAAAGACTGAT 1628
Db      510  GlyLysPheSerLysSerAlaAenLeuLeuCysThrGluGluValAenPheGlnAenAsp 529
QY      1629  GTATCTGGAACTGTGTGTATAGTATTCAGGATACACACAGATGTGAAGCTGCAATCTG 1688
Db      530  LysPheGlyAsnCysGly-----GlnArgCysProPhePheAspIle 543
QY      1689  CAGTGGGAAATTAATATGTAATATGATAGTAAATTTTATATCAAAATTCAGAGGCC 1748
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Db      564  AspIleGlnTyrThrTyrLeuGlyGlyHisValCysLeuSerAlaHis---AlaArgAsn 582
QY      1809  CATGCACACAGCCAAAGATGTGGATATAAAGATGGAACACTTCTTGTGTTCAAATAAGTT 1868
Db      583  AlaSerLysGlnLeuGlyThrTyrThrGluAspIleThrAlaCysGlyGlnLysVal 602
QY      1869  TGCAAGAAATCAAGATGTGTGAGTTCTTCACTACTTGGTTATGATTCTACTACTGACAAA 1928
Db      603  CysArgSerArgGlyCysArgTyrLeuSerGluLeuAenIleThrLysCysThrThrAsn 622
QY      1929  TGCAATGATAGAGTGTATGCAATAAACAAGACACTGTCACTGTAGTGTCTTCAATTTA 1988
Db      623  CysGlyGlnAenGlyIleCysAsnAspArgPheHisCysGlnCysAspProGlyTyrAla 642
QY      1989  CTTCCAGATTGC-----TCAGTTCAATCAGATCTATGGCTGTGGAGTATTCAGACT 2042
Db      643  ProProAspCysAspProSerMetSerSer-----ProGlyGlySerIleAspAsp 659
QY      2043  GGCAATTTTCCACTGTA-----GCTATACCAAGCCAGACTCCTCGAAAGCGCTACATT 2096
Db      660  GlyPheThrLeuSerValAspLysSerValProLeu---PheProLysGlnArgAlaAla 678
QY      2097  GAGAACATTTACCATTCACAAACCAATCAGATGCCATTTTCTTATTCTTCTTCTTT 2156
Db      679  ProLys-----AsnAenGlyLeuLeuIleSerPheTyrIlePheSerProLeuLeu 695
QY      2157  ATTATTTCTGTCTACTGATTGCTATTAATGCTGAAGTTAAATTTCCAAAGGAAAAATGG 2216
Db      696  IleuIleAlaIle-----ValSerLeuLysTrpAsnLysMetLysArgPheTrp 712
QY      2217  AGA-----ACTGAGGACTATTTCAGCCGATGAGCAA 2246
Db      713  SerLysValGlyThrValSerSerArgSerIleSerGluAsp---SerSerSerAsnAsn 731
QY      2247  CCTGAAAGTGAAGT 2261
Db      732  SerGlnSerGlnSer 736

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S18968
Cytirestin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: I48784; S18968
R;Senftleben, A.; Wallat, S.; Lemaire, L.; Heinlein, U.A.O.
Dev. Growth Differ. 36: 49-58, 1994
A;Title: Pre and postmitotic germ cell specific expression of TAZ83, a gene encoding a p
A;Reference number: I48784
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-823 <RES>
A;Cross-references: UNIPROT:Q62287; EMBL:X64227; NID:954264; PID:954265
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C;Superfamily: mouse meltrin alpha; disintegrin homology
F;395-480/Domain: disintegrin homology <DIS>

Alignment Scores:
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Score: 1292.00 Matches: 256
Percent Similarity: 55.01% Conservative: 156
Best Local Similarity: 34.18% Mismatches: 303
Query Match: 26.94% Indels: 34
DB: 2 Gaps: 15

US-10-054-683-18 (1-2640) x S18968 (1-823)
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Db      5  LeuPheLeuValLeuSerTyrLeuGlyGlnValIleAlaAaGlyLysAspValGluThr 24
QY      135  TTACTGTGCAAAATACAGTTCGCGAGAAATACGGTCAATTAATAAGGAAGGA----- 188

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Qy 189 ATTGAATCGCAGGATCCTACAAATTTGAATTAAGAGGAAACCATATCTACTGTCAATTTA 248
Db 45 AlaGluThrGlnValThrTyValValThrIleGluGlyLysAlaTyThrLeuGlnLeu 64
Qy 249 ATGCAAAAACCTTTTACCCCATAAATTTAGAGTTTACAGTTATAGTGGCAGAGAAATT 308
Db 65 GluLysGlnSerPheLeuHisProLeuPheGlyThrTyThrLeuArgAspLysLeuGlyThr 84
Qy 309 ATGAACACCTTGCACCAAGATTTTCAAAATTTCTGCCACTACCAAGGGTATATTGAAGGT 368
Db 85 LeuGlnProTyPheSerLeuValLysThrHisCysPheTyThrGlnGlyHisAlaLysGlu 104
Qy 369 TATCCAAAATCTGTGGTGTAGTGGTACATGATGATGATGATGATGATGATGATGATGATGAT 428
Db 105 IleProValSerThrValThrLeuSerThrCysSerGlyLeuArgGlyLeuGlnLeu 124
Qy 429 GAAATGTTAGTTATGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAAACATGTAATT 488
Db 125 GluAsnIleThrTyGlyIleGluProLeuGluSerSerAlaThrPheGluHisIleLeu 144
Qy 489 TACCAAGTAAACATAGAAGCAGATGTTTCC-----TTATATAAT 530
Db 145 TyrGluIleLysAsnAsnLysIleAspTySerProLeuLysGluAsnPheAlaAsnSer 164
Qy 531 GAGAAGGATATTGAATCAAGAGATCTGCTCTTAAATTTACAAAGCGCAGAGCCACACAA 590
Db 165 GluGlnGluSerGlnSerTyArgIleLeuValLysProGluLysGlySerAsnSerThr 184
Qy 591 GATTTTGCAAAGTATATAGAAATGCATGTTATAGTTGAAACAAATTTGTAATATCATATG 650
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Qy 651 GGCTCTCATCAACTGTTGCTGCTCAAAAGTTTCCAGTTGATGATGATGATGATGATGATGAT 710
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Qy 891 TCAAAATATCTGTGTCACCACTTCAAGGGAAGATGTCATGCAAACTATGCAAGAGGT 950
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Qy 1191 CCTCGCTTAGATCCTTTTCAACACAGCAA-----GCAGTGTGTGTTAATGCAAAAGCTG 1244

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Qy 1245 GAACAGCAGAGAGGAGTGTGACTGTGGGACTCAACAGGATTTGTCCCTTATTGGGAGAAACA 1304
Db 405 GluValProGluGlnCysAspCysGlyProGluThrCysThr-----HisLeuLys 422
Qy 1305 TGCTGTGATATTGCCCATGTAGATTTAAAGCCGGTTCAAACTGTGCTGTGAAGGACCATGTC 1364
Db 423 CysCysAsnProLysAspCysThrLeuIleAspAlaGlnCysGlyThrGlyProCys 442
Qy 1365 TGGCAA-----AACTGCTCTATTATGTCAAAAGAAAGATGTGTAGSCCTTCTCTTTGAA 1418
Db 443 CysAspLysArgThrCysThrIleAlaGluArgGlyArgLeuCysArgLysSerLysAsp 462
Qy 1419 GAATGGCAGCTCCCTGAATATTGCAATTTGATGATCATCTGCATCATGCCAGAGAAACCATAT 1478
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Qy 1479 GTTCAGACTGGGCATCCGTGTGAGTCAATCAATGATCTGTATAGATGAGTTTGTATG 1538
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Qy 1539 AGTGGGATAAAACAAATGTACAGACATTTTGGCAAGAAAGTGTAGTTTGGCCCTTCA--- 1595
Db 503 AspProAspArgGlnCysThrAspLeuPheGlyLysTyThrAlaLys---GlyProAsnTy 521
Qy 1596 GAATGTATTCTCACCTTAAATCAAGACTGATGTATCTCGAAACTGTGGTATATAAGTAT 1655
Db 522 ValCysAlaGlnGluValAsnLeuGlnAsnAspLysPheGlyAsnCys----- 537
Qy 1656 TCAGGATACACAGTGTGAAGCTGACATCTGCAGTGGCGGAAATTAATTAATGTAATAT 1715
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Qy 1776 CATCTCTGCATCTGCTGGAATTTGCGAGTGTATGTCAGACAGCCAAAGATGTGATA 1835
Db 576 GlnValCysValSerAlaHisLeuArgSerGlnThrGlyThrArgAspAspThrTyThrVal 595
Qy 1836 AAAGATGGAATCTTGTGTTCAATTAAGTTTGCAGGAATCAAGATGTGTGAGTTCT 1895
Db 596 HisAspGlyThrValCysGlySerGlyGlnValCysPheArgGlyAspCysLeuArgVal 615
Qy 1896 TCATACTTG-----GGTATGATTGT---ACTACTGCAAAATGCAATGATAGAGGTGA 1946
Db 616 HisValLeuArgGlyThrArgGluCysGluAlaAspAspLysCysGlnGlyHisGlyIle 635
Qy 1947 TGCAATAACAAAGACACTGCTACTGTAGTGTCTCATATTTTACTCCAGATTTGCTCAGTT 2006
Db 636 CysAsnAsnLeuAsnAsnCysGlnCysGluSerGlyPheAlaProProGluCysAspMet 655
Qy 2007 CAATCAGATCTATGGCTGTGGAGTATTACAGAGTGGCAATTTTCCACCTAGTGTATA 2066
Db 656 ThrProSerSer---ProGlyGlySerMetAspAspGlyPheTrpLeuProPheAspLys 674
Qy 2067 CAGCCAGACTCCTGAAAGGCGCTACATTGAGAACATTTTACCATTCCCAACCAATGAGA 2126
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Qy 2127 TGGCCATTTTCTTATTCTCTTCTTTTATTATTATTCTGTGTACTGTTGTTGTTTATATG 2186
Db 693 IleSerPheTyThrLeuLeuProPheLeuValVal-----LeuAlaPheMet 708
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Qy 2247 CCTGAAGTGTAGAGTGAACTAAAGG 2273
Db 729 HisLysGluGluAlaPheAsnArgGly 737

207	ValLeuProGln-----ThrArgTyrValGluLeuPheIleValAlaAspLysGlu	223
636	TTGTATAATCATATGGGGTCTGATACAACTGTTGTGGCTCAAAAGATTTTCCAGTGTGATT	695
224	ArgTyrAspMetMetGlyArgAsnGlnThrAlaValArgGluGluMetIleLeuLeuAla	243
696	GGATTGACGAATGCTATTTTTTGTTCATTTAATATTACAAATATTCTGTCTTCATTGGAG	755
244	AsnTyrLeuAspSerMetTyrIleMetLeuAsnIleArgIleValLeuValGlyLeuGlu	263
756	CTTTGGATAGATGAATAAATAATTCACACCTGGGAGAGCTAATGATGTTATTACACACA	815
264	IleTrpThrAsnGlyAsnLeuIleAsnIleValGlyGlyAlaGlyAspValLeuGlyAsn	283
816	TTTTTAAGATGGAAACATCTTATCTTGTGTTTAA---CGTCCTCATGATGGCAATTTTAA	872
284	PheValGlnTrpArgGluLysPheLeuIleThrArgArgArgHisAspSerAlaGlnLeu	303
873	CTTTGTTTACAGAGAAAGTCAAAATATTATGTTGGTGCACACCTTCAAGGGAAGATGTGTGAT	932
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933	GCAAACTATCCAGAGGTGTTGTTCTGCACCCACAGAACCAATAGTCTGGAATCACTTGCA	992
324	ArgSerHisAlaGlyGlyIleAsnValPheGlyGln---IleThrValGluThrPheAla	342
993	GTTATTTTACGTCATTAATTATGAGCCTTAGTATGGGATCACTTATGATGACATTAACAAA	1052
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1053	TGCCAGTGTCTCAGGAGCTGTCTGCATTATGAATCCAGAGCAATTCATTTCAGTGTGTG	1112
363	CysSerCysGlyAlaLysSerCysIleMetAsnSerGlyAla-----SerGlySer	379
1113	AAGATCTTTTAGTAATCTGCAGCTTCGAAAGACTTTGCACATTTTATTTCAAAGCAGAGTCC	1172
380	ArgAsnPheSerSerCysSerAlaGluAspPheGluLysLeuThrLeuAsnLysGlyGly	399
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1233	AATGCAAGCTGGAAGCAGGAGAGTGTGACTGTGGGACTGAACAGGATTTGTGCCCTT	1292
419	AsnLysLeuValAspAlaGlyGluGluCysAspCysGlyThrProLysGluCysGluLeu	438
1293	ATTGGAGAACATGCTGTGTGATATTGCCCATGATAGATTAAAGCCGGTTCAAACCTGTGCT	1352
439	-----AspProCysCysGluGlySerThrCysLysLeuLysSerPheAlaGluCysAla	456
1353	GAAGGACCATGTCGCGAAACTGCTATTATTATGTCAAAGAAAGATGCTAGGCCCTTCC	1412
457	TyrGlyAspCysCysLysAspCysArgPheLeuProGlyThrLeuCysArgGlyLys	476
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1533	TGTATGAGTGGGATAAACAATGTACAGACACATTTGGCAAGAGTAGAGTTTGGCCCT	1592
517	CysGlnTyrTyrAspAlaGlnCysGlnValIlePheGlySerLysAlaLysAlaPro	536
1593	TCGAATGTTATTCTCACCTTAATTCAAAGACTGATGTATCTCGAAACTGTGGTATAAGT	1652
537	LysAspCysPheIleGluValAsnSerLysGlyAspArgPheGlyAsnCysGlyPheSer	556
1653	GATTTCAGGATACACACAGTGTGAAGCTGCAATCTCGCAGTGGCGAAATTAATATGTAAA	1712

QY 384 GTGATGTTAGCACATGTACTGCGACTCAGGCGCTACTACAGTTTGAATAATGTTAGTTAT 443
Db : : : : :
10 LeuLeuLeuAlaThrValLeuAspLeuArgGlyLeuLeuHisLeuGluAsnAlaSerTyr 29
QY 444 GGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAACATGTAATTTACCAAGTA----- 497
Db : : : : :
30 GlyIleGluProLeuGlnMetSerHisPheGluHisIleIleTyrArgMetAspAsp 49
QY 498 -----AAACATAAGAACAGCAGATGTTCTCTTATATATAGAGAGGATATTGAATCA 548
Db : : : : :
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QY 549 AGA-----GATCTGTCCTTTAAATTA 569
Db : : : : :
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204 CysSerArgSerHisAlaGlyGlyIleAsnValPheGlyGln---IleThrValGluThr 222
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Db : : : : :
280 GlyGlyAsnCysLeuLeuAsnIleProLysProAspGluAlaTyrSerAlaProSer--- 298
QY 1227 TGTGGTAAATGCAAGCTGGAAGCAGGAGAGTGTGACTGTGGAGCTGGAACAGGATGT 1286
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299 CysGlyAsnLysLeuValAspAlaGlyGluCysAspCysGlyThrProLysGluCys 318
QY 1287 GCCCTTATTGAGAAACATGCTGTGATTTATGCCACATGTAGATTTAAAGCGGTTCAAC 1346
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337 CysAlaTyrGlyAspCysCysLysAspCysArgPheLeuProGlyGlyThrLeuCysArg 356

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357 GlyLysThrSerGluCysAspValProGluTyrCysAsnGlySerGlnPheCysGln 376
QY 1467 GAAACCACTATGTTACAGACTGGGCATCCGTGTGGACTGAATCAATGGAATCTGTATAGAT 1526
Db : : : : :
377 ProAspValPheIleGlnAsnGlyTyrProCysGlnAsnAsnLysAlaTyrCysTyrAsn 396
QY 1527 GGAGTTTGTATGAGTGGGATAAACAATGTACAGACACATTTGGCAAGAGTACAGTTT 1586
Db : : : : :
397 GlyMetCysGlnTyrTyrAspAlaGlnCysGlnValIlePheGlySerLysAlaLysAla 416
QY 1587 GGCCCTTCAGAATGTTATCTCACCTTAATTAAGACTGATGATATCGAAAACGTGGT 1646
Db : : : : :
417 AlaProLysAspCysPheIleGluValAsnSerLysGlyAspArgPheGlyAsnCysGly 436
QY 1647 ATAAGTCAATTCAGATACACACAGTGTGAA----- 1676
Db : : : : :
437 PheSerGlyAsnGluTyrLysLysCysAlaThrGlyLeuSerLeuLysPheHisAlaPro 456
QY 1676 ----- 1676
Db : : : : :
457 PheLeuSerThrMetLeuGlnGluAlaValArgGlnThrGlyThrTyrLeuGlyGlySer 476
QY 1677 -----GCTGACAATCTGCGAGTGGCA 1697
Db : : : : :
477 ValCysCysMetLysSerAspCysArgIleValThrLeuValLysAsnAlaLeuCysGly 496
QY 1698 AATTAATATGTAATATGTTAGTAAATTTTATTACAAATTTCCNAGAGCCACTATTATT 1757
Db : : : : :
497 LysLeuGlnCysGluAsnVal-----GlnGluIleProValPheGlyIleVal 512
QY 1758 TATGCCAACATAAGT-----GGACATCTCTGCAATTCGTGTGAATTT 1799
Db : : : : :
513 ProAlaIleIleGlnThrProSerArgGlyThrLysCysTrpGlyValAspPheGlnLeu 532
QY 1800 GCCAGTGATCATCGACAGCCAAAAGATGTGGATAAAGATGGAATCTTGTGGTTCA 1859
Db : : : : :
533 GlySerAspValProAspProGly-----MetValAsnGluGlyThrLysCysGlyAla 550
QY 1860 AATAAGTTTGCAGGATCAAGATGTGTGAGTCTTCTCATCTGTTGGTTATGTTGTTACT 1919
Db : : : : :
551 GlyLysIleCysArgAsnPheGlnCysValAspAlaSerValLeuAsnTyrAspCysAsp 570
QY 1920 ACTGAC---AAATGCAATGATAGAGGTGATGCAATAACAAAGACACTGCTCAGTGTAGT 1976
Db : : : : :
571 ValGlnLysLysCysHisGlyHisGlyValCysAsnSerAsnLysAsnCysHisCysGlu 590
QY 1977 GCTTCATATTTACTCCAGATGCTCAGTTCAATCAGATCTATGCGCTGGTGGAGTATT 2036
Db : : : : :
591 AsnGlyTrpAlaProAsnCysGluThrLysGly-----TyrGlyGlySerVal 607
QY 2037 GACAGTGGC 2045
Db : : : : :
608 AspSerGly 610

RESULT 12

S60257

meltrin alpha - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: S60257

R;Yagami-Hironaka, T.; Sato, T.; Kurisaki, T.; Kamijo, K.; Nabeshima, Y.I.; Fujisawa-Seh-

Nature 377, 652-656, 1995

A;Title: A metalloprotease-disintegrin participating in myoblast fusion.

A;Reference number: S60257; MUID:96026308; PMID:7566181

A;Accession: S60257

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-903 <VAG>

A;Cross-references: UNIPROT:Q61824; EMBL:D50411; NID:gl054586; PIDN:BAA08912.1; PID:gl05-

C;Superfamily: mouse meltrin alpha; disintegrin homology

F;421-503/Domain: disintegrin homology <DIS>

fertilin alpha precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C/Accession: I49281
R:Wolfsberg, T.G.; Straught, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.
Dev. Biol. 169, 378-383, 1995
A>Title: ADAM, a widely distributed and developmentally regulated gene family encoding m
A/Reference number: I48100; MUID:95269891; PMID:7750654
A/Accession: I49281
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-600 <RES>
A/Cross-references: EMBL:U22056; NID:g965009; PID:AAA74920.1; PID:g965010
C/Genetics:
C/Superfamily: disintegrin homology
F:246-326/Domain: disintegrin homology <DIS>
F:180/Active site: Glu #status predicted

Alignment Scores:
Pred. No.: 7,21e-51 Length: 600
Score: 795.00 Matches: 193
Percent Similarity: 44.86% Conservative: 82
Best Local Similarity: 31.48% Mismatches: 256
Query Match: 16.58% Indels: 82
DB: 2 Gaps: 20

US-10-054-683-18 (1-2640) x I49281 (1-600)

QY 552 GATCTGTCCTTTAAATACAAAGCGCAGAGCCAGCA----- 590
DB 20 AsphrSerHisProArgSerArgLysProAspLeuValLeuThraspTyr 39
QY 591 ---GATTTTCCAAAGTATAGAAATCATCTTATAGTGAACAAATGTAATCAT 647
DB 40 TrpSerHisThrLysTyrValGluMetPheValValAlaHisGlnArgPheGlnMet 59
QY 648 ATGGGGTCTGATCAACACTGTTCGCTCAAAAGCTTTTCAGTTGATGGATGACCAAT 707
DB 60 TrpGlySerAsnIleAsnGluThrValGlnAlaValMetAspIleIleAlaLeuAlaAsn 79
QY 708 GCTATTTTGTGTTTCAATTAATTAATTAATTAATTCGCTTCATGAGCTTTGATAGAT 767
DB 80 SerPheThrArgGlyIleAsnThrGluValValLeuValGlyLeuGluIleTrpThrGlu 99
QY 768 GAAATAAATGCAACCACTGGAGAGCTAATGAGTTATACACATTTTAAAGATGG 827
DB 100 GlyAspProIleGluValProValAspLeuGlnThrThrLeuArgAsnPheAspTyr 119
QY 828 AAAACATCTTATCTGTTTACGT---CCTCATGATGGCATTCTTACTTTGTTTACAGA 884
DB 120 ArgGlnGluLysLeuValGlyArgValArgHisAspValAlaHisLeuIleValGlyHis 139
QY 885 GAAAGTCAATATATGTTGGTCAACCTTTCAGGGAGAGATGTTGATGCAACTATGCA 944
DB 140 ArgProGlyGluAsnGluGlyGlnAlaPheLeuArgGlyAlaCysSerGlyGluPheAla 159
QY 945 GGAGGTGT---GTTCTGCACCCAGAACCAATAGTCTGGAATCACTTGCAGTTATTTTA 1001
DB 160 AlaValGluAlaPheHisHisGluAspValLeuLeu-----PheAlaLeuMet 177
QY 1002 GCTCAATATTAGACCTTTAGTATGGGATCACTTATGATGATCAATTAACAAATGCCAGTC 1061
DB 178 AlaHisGluLeuGlyHisAsnLeuGlyIleGlnHisAspHis----- 191
QY 1062 TCAGAGCTGCTGCATTAATGAATCCAGAACCAATTCATTTTCAGTGGTGTGAAGATC--- 1118
DB 192 -----ProThrCysThrCysGlyProLysHisPheCysLeuMetGlyGluLysIleGly 209
QY 1119 -----TTTAGTAACGTCAGCTTCAAGACTTTGACATTTTATTTTCAAGCAG 1166
DB 210 LysAspSerGlyPheSerAsnCysSerSerAspHisPheLeuArgPheLeuHisAspHis 229

QY 1167 AAGTCCCACTGCTTCCAAATCAGCTCCCTAGATCCTTTTCAACAGCAAGCAGTG 1226
DB 230 ArgGlyAlaCysLeuLeuAspGluProGlyArgGlnSerArgMetArgAlaAlaAsn 249
QY 1227 TGTGGTAATCAAGCTGGAAGCAGAGAGGAGTGTGACTGTGGGACTGAACAGGATGT 1286
DB 250 CysGlyAsnGlyValValGluAspLeuGluGluCysAspCysGlySerAspCysAsp 268
QY 1287 GCCCTTTATGGAGAACATGCTGTGTATATGCCACATGTAGATTTAAAGCCGGTCCAAAC 1346
DB 269 -----SerHisProCysCysSer---ProThrCysThrLeuLysGluGlyAlaGln 284
QY 1347 TGTGCTGAAGGACCATGCTGCGAAAACCTCTATTATTATGTCAAAAGAAAGATGTAGG 1406
DB 285 CysSerGluGlyLeuCysCysTyrAsnCysThrPheLysLysLysGlySerLeuCysArg 304
QY 1407 CTTTCCTTTGAAGATGCGACCTCCCTGAATATTGCAATGGAATCATCTGCATCATGCCCA 1466
DB 305 ProAlaGluAspValCysAspLeuProGluTyrCysAspGlySerThrGlnGluCysPro 324
QY 1467 GAAACCACTATGTTCCAGACTGGGCATCGGTGTGAGCTGAATCAATGGATCTGTATAGAT 1526
DB 325 AlaAsnSerIleMetGlnAspGlyThrGlnCysAsp---ArgIleTyrTyrCysLeuGly 343
QY 1527 GGAGTTTGTATGAGTGGGATAAACAATGTACAGACACATTTGGCAAGAGTAGAGTTT 1586
DB 344 GlyTyrCysLysAsnProAspLysGlnCysSerArgIleTyrGlyTyrProAlaArgSer 363
QY 1587 GGCCTTTCAGATGTTTATCTACCTTAATTCAGAGCTGATGTATCTGAAACTGTGGT 1646
DB 364 AlaProGluGluCysTyrIleSerValAsnThrLysAlaAsnArgPheGlyAsnGly 383
QY 1647 ATAAGTGATTCAGGA-----TACACACAGTGTGAAGCTCAACATCTGCGAGCGGA 1697
DB 384 HisProThrSerAlaAsnPheArgTyrGluThrCysSerAspGluAspValPheCysGly 403
QY 1698 AATTAATATGT-----AATATGTAGTGAATATTT-----TTATTA 1733
DB 404 LysLeuValCysThrAspValArgTyrLeuProLysValLysProLeuHisSerLeuLeu 423
QY 1734 CAATTCAGAGGCC-----ACTATTATTATGCCAACATAAGTGGACAT 1778
DB 424 GlnValProTyrGlyGluAspTyrCysTrpSerMetAspAlaTyrAsnIleThrAsp--- 442
QY 1779 CTCTGCACTGCTGGAAATTTGCCAGTGATCATGCAGACAGCCAAAGATGTGCTATAAA 1838
DB 443 -----ValProAspAspGlyAsp-----ValGln 450
QY 1839 GATGGAACCTTCTGTTGTTCAATAAGTTTGCAGGAATCAAGATGTGTGATCTCTTCA 1898
DB 451 SerGlySerPheCysAlaProAsnLysValCysMetGluTyrIleCysThrGlyArgGly 470
QY 1899 TACTTGGTTTATCATTTGT---ACTACTGACAAATGCAATGATAGAGTGTATGCAATAAC 1955
DB 471 ValLeuGlnTyrAsnCysGluProGlnGluMetCysHisGlyAsnGlyValCysAsnAsn 490
QY 1956 AAAAAGCACTGTCATGTAGTCTTCATATTTTACTCCAGATTTGCTCAGTTTCAATCATAG 2015
DB 491 PheLysHisCysHisCysAspAlaGlyPheAlaProProAspCysSerSerProGlyAsn 510
QY 2016 CTATGGCTGCTGGAGTATTGACAGTGGCAATTTTCCACCTGATAGTATACCAGCC--- 2072
DB 511 -----GlyGlySerValAspSerGly-----ProValGlyLysProAlaAsp 524
QY 2073 -----AGACTCCTCGAAAGCGCTACATTGAGAAC 2102
DB 525 ArgHisLeuSerLeuSerPheLeuAlaGluLysSerProAspAspLysMetGluAspGlu 544
QY 2103 ATTTACCAATTCACCAACCAATGAGATGGCCATTTTCTTATCATCTCTTTCTTTATTAT 2162
DB 545 GluValAsnLeuLysValMet-----ValLeuValValProIlePheLeuVal 560
QY 2163 TTCTGTGCTACTGATTCGTATATGTTGTAAGTTAAATTTCCAAAGGAAAAAATGGAAGACT 2222

Db 561 ValLeuLeuCysCysLeuMetLeuLeuAlaTyrTrpSerGluValGlnGluValVal 580
Qy 2223 GAGGACTATTCAAGCGATGACCACTGAAAGTGAGAGT 2261
Db 581 SerProSerSerSerGluSerSerSerSerSer 593
RESULT 14
A60385
monocyte surface antigen MS2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60385
R;Yoshida, S.; Setoguchi, M.; Higuchi, Y.; Akizuki, S.; Yamamoto, S.
Int. Immunol. 2, 585-591, 1990
A;Title: Molecular cloning of cDNA encoding MS2 antigen, a novel cell surface antigen st
A;Reference number: A60385; MUID:91197896; PMID:1982220
A;Accession: A60385
A;Molecule type: mRNA
A;Residues: 1-826 <YOS>
A;Cross-references: UNIPROT:Q8R3D3; EMBL:X13335
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Keywords: glycoprotein; surface antigen; transmembrane protein
F;1-14/Domain: signal sequence #status predicted <SIG>
F;402-484/Domain: disintegrin homology <DIS>
F;659-683/Domain: transmembrane #status predicted <TM>
F;330/Active site: Glu #status predicted
Alignment Scores:
Pred. No.: 1e-48 Length: 826
Score: 766.00 Matches: 189
Percent Similarity: 49.11% Conservative: 116
Best Local Similarity: 30.43% Mismatches: 260
Query Match: 15.97% Indels: 56
DB: 2 Gaps: 25
US-10-054-683-18 (1-2640) x A60385 (1-826)
Qy 204 TCCTACAAATGTGAATTGAAGGAAACCATATCTGTGTAATTAATGCAAAAAAATTT 263
Db 56 SerTyrAlaLeuGlyThrSerGlyHisValPheThrLeuHisLeuArgLysAsnArgAsp 75
Qy 264 TTACCCCATATTTAGAGTTTACAGTTATAGT-----GGCAGAGAATTTGAAA 314
Db 76 LeuLeuGlySerSerTyrThrGluThrTyrSerAlaAlaAsnGlySerGluValThrGlu 95
Qy 315 CCACCTTGACCAGATTTTCTGCAATTTCTGCACCTTACCAGGGTATATTGAAGGTATCCA 374
Db 96 GlnLeuGlnGlu-----GlnAspHisCysLeuTyrGlnGlyHisValGluGlyTyrGlu 113
Qy 375 AAATCTGTGTGTGTTAGTGTACATGTACTGTGGAGCTCAGGGCGCTACTACAGTTTGAATAAT 434
Db 114 GlySerAlaAlaSerIleSerThrCysAlaGlyLeuArgGlyPhePheArgValGlySer 133
Qy 435 GTTAGTTATGGAATAGAACCCCTGGAGCTTTCAGTTGGCTTTGAAACATGTAATTTACCAA 494
Db 134 ThrValHisLeuIleGluProLeuAspAlaAspGluGlyGlnHisAlaMetTyrGln 153
Qy 495 GTAAACATAGAAGCAGATGTTCTCTTATATATAGAGGATATTGATCAAGAGAT 554
Db 154 AlaHisLeuGlnGlnLysAlaGlyThrCysGlyValLysAspThrAsnLeuAsnAsp 173
Qy 555 CTG-----TCCTTAAATATACAAAGCGCAGAGCCAGCAAGATTTT----- 596
Db 174 LeuGlyProArgAlaLeuGluIleTyrArgAlaGlnProArgAsnTrpLeuIleProArg 193
Qy 597 ---GCAAGATATAGAAATGATGTTATGTTGAAACAAATGTTGTAATCATATGCGG 653
Db 194 GluThrArgTyrValGluLeuTyrValValAlaAspSerGlnGluPheGlnLysLeuGly 213
Qy 654 TCTGTACAACTGTTGCGCTCAAAAGTTTCCAGTTGATGATGAGTTCAGTATTTAT 713
Db 214 Ser---ArgGluAlaValArgGlnArgValLeuGluValValAlaAsnHisValAspLysLeu 232

Qy 714 TTTGTTTCATTTAATATTACAAATTTCTCTCTTCATTGGAGCTTTGGATAGATGAAAT 773
Db 233 TyrGlnGluLeuSerPheArgValValLeuValGlyLeuGluIleTrp---AsnLysAsp 251
Qy 774 AAAATTGCAACCACTGGAGAAGCTAATAGCTTATTACACACATTTTAAAGATGAAACA 833
Db 252 LysPheTyrIleSerArgTyrAlaAsnValThrLeuGluAsnPheLeuSerTrpArgGlu 271
Qy 834 TCTTATCTCTGTT---TTACGTCCTCATGATGTGGCATTTTACTGTGTTTACAGAGAAAAG 890
Db 272 GlnAsnLeuGlnGlyGlnHisProHisAspAsnValGlnLeuIleThr-----Gly 288
Qy 891 TCAATATATGTTGGTCAACCTTT-----CAAGGGAAGATGTGTGATGCAAAAC 938
Db 289 ValAspPheIleGlySerThrValGlyLeuAlaLysValSerAlaLeuCysSerArgHis 308
Qy 939 TATGCAAGGAGTGTGTTCTGCACCCAGAACCATAGTCTGGAATCCTTGGAGTTATT 998
Db 309 -----SerGlyAlaValAsnGlnAspHisSerLysAsnSerIleGlyValAlaSerThr 326
Qy 999 TTAGCTCAATTTAGCCCTTAGTATGGGATCACTTATGAT---GACATTAAACAAATGC 1055
Db 327 MetAlaHisGluLeuGlyHisAsnLeuGlyMetSerHisAspGluAspIleProGlyCys 346
Qy 1056 CAGTGC-----TCAGGAGCTGTGCTGATTTATGATCCAGAAAGCAATTCATTTC 1103
Db 347 TyrCysProGluProArgGluGlyGlyCysIleMetThr---GluSerIleGlySer 365
Qy 1104 AGTGTGTGAAGATCTTTAGTAATCGAGCTTCGAGACTTTGCACATTTTATTTCAAAG 1163
Db 366 LysPheProArgIlePheSerArgCysSerLysIleAspLeuGluSerPheValThrLys 385
Qy 1164 CAGAAGTCCCAAGTGTCTTCAATCAGCCCTGCTAGATCCTTTTTCACCAAGCAAGCA 1223
Db 386 ProGlnThrGlyCysLeuThrAsnValProAspValAsnArgPheVal---GlyGlyPro 404
Qy 1224 GTGTGTGTAATCAAGCTGGAAGCAGAGAGAGTGTGACTGTGGAGCTGACACAGAT 1283
Db 405 ValCysGlyAsnLeuPheValGluHisGlyGluGlnCysAspCysGlyThrProGlnAsp 424
Qy 1284 TGTGCTCTTATGGAGAAACATCTGTGATATTGCCACATGTAGATTTAAAGCCGTTCA 1343
Db 425 CysGln-----AsnProCysCysAsnAlaThrThrCysGlnLeuValLysGlyAla 441
Qy 1344 AACTGTGTGGAAGCAGCTGCGAAACTGTCTATTATGTCAAAAAGAAAGATGTGT 1403
Db 442 GluCysAlaSerGlyThrCysCysHisGluCysLysValLysProAlaGlyGluValCys 461
Qy 1404 AGCCCTTCCCTTTGAAGAATCGCACTCCCTCGAATATTGGCAATGATCATCTGCATCATGC 1463
Db 462 ArgLeuSerLysAspLysCysAspLeuGluGluPheCysAspGlyArgLysProThrCys 481
Qy 1464 CAGAAAACCACTATGTTGAGCTGGCATCCGTGTGGACTGAATCATGATGATCTGTATA 1523
Db 482 ProGluAspAlaPheGlnGlnAsnGlyThrProCys-----ProGlyGlyTyrCysPhe 499
Qy 1524 GATGGAGTTTGTATGATGGGGATAAACAATGTACAGACACATTTGGCAAGAAGTAGAG 1583
Db 500 AspGlySerCysProThrLeuAlaGlnGlnCysArgAspLeuTrpGlyProGlyAlaArg 519
Qy 1584 TTTGGCCCTTCAGAAATGTTTCTCACCTTAATTCAAAGACTGATGTATCTGGAACCTGT 1643
Db 520 ValAlaAlaAspSerCysTyrThrPhe-----SerIleProProGlyCys 534
Qy 1644 ---GGTATAGTGAATTCAGGATACACACAGTGTGAAGCTGACAATCTGCAGTGGGAAAA 1700
Db 535 AsnGlyArgMetTyrSerGlyArgIleAsn-----ArgCysGlyAla 548
Qy 1701 TTAATATGAAATATCTAGGTAATTTTATTACAAATTCAGAGCCCATTTATTTAT 1760
Db 549 LeuTyrCysGluGlyGlnLys-----ProLeuGluArgSerPheCysThrPhe 565

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 10, 2005, 21:24:40 ; Search time 491.5 Seconds

(without alignments)
6181.034 Million cell updates/sec

Title: US-10-054-683-18

Perfect score: 4796

Sequence: 1 catctgcacttccaaactgc.....actgttaccatttcaaaaaa 2640

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2 i/USPTO spool_p/US10054683/runat 10012005 174510 15496/app query fasta_1.2823
-DB=UniProt_02 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomum2 -TRANS=human40.cdi -LIST=45
-LOCALALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10054683 @CNG 1.1 518 @runat 10012005 174510 15496 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3969.5	82.8	735	1 AD02 HUMAN	Q9965 homo sapien
2	3690.5	76.9	735	1 AD02 MACFA	Q28478 macaca fasc
3	3065.5	63.9	579	2 Q6P2G0	Q6p2g0 homo sapien
4	3065.5	63.9	579	2 AAH64547	Aah64547 homo sapi
5	2820	58.8	735	2 Q866A8	Q866a8 sus scrofa
6	2723	56.8	745	1 AD02 BOVIN	O77780 bos taurus
7	2685	56.0	751	1 AD02 RABIT	Q28660 oryctolagus
8	2479.5	51.7	717	1 AD02 RAT	Q63202 rattus norv
9	2453.5	51.2	735	1 AD02 MOUSE	Q60718 mus musculus
10	2326	48.5	735	1 AD02 CAVPO	Q60411 cavia porce
11	1586.5	33.1	746	1 AD18 MACFA	Q95194 macaca fasc
12	1582.5	33.0	739	1 AD18 HUMAN	Q9y3q7 homo sapien
13	1524.5	31.8	787	2 Q8TC27	Q8tc27 homo sapien
14	1524.5	31.8	787	2 AAQ89099	Aaq89099 homo sapi
15	1519.5	31.7	787	2 Q8TC42	Q8tc42 homo sapien
16	1493.5	31.1	715	2 Q6UXJ9	Q6uxj9 homo sapien

17	1493.5	31.1	715	2 AAQ88687	Aaq88687 homo sapi
18	1437.5	30.0	750	2 Q6P901	Q6p901 mus musculus
19	1437.5	30.0	750	2 AAH60983	Aah60983 mus muscu
20	1433	29.9	750	2 Q8K410	Q8k410 mus musculus
21	1384.5	28.9	756	2 Q28483	Q28483 macaca fasc
22	1373	28.6	730	2 Q80Y08	Q80y08 mus musculus
23	1367.5	28.5	677	2 Q8BJ80	Q8bj80 mus musculus
24	1366.5	28.5	719	1 AD18 MOUSE	Q9r157 mus musculus
25	1365.5	28.5	736	2 Q28482	Q28482 macaca fasc
26	1293	27.0	822	2 Q62287	Q62287 mus musculus
27	1292	26.9	740	2 P70534	P70534 rattus norv
28	1288	26.9	777	2 Q60472	Q60472 cavia porce
29	1237	25.8	771	2 Q8CDV5	Q8cdv5 mus musculus
30	1237	25.8	771	2 Q9D4F0	Q9d4f0 mus musculus
31	1217	25.4	819	1 AD09 HUMAN	Q13443 homo sapien
32	1206	25.1	751	2 Q60816	Q60816 mus musculus
33	1174	24.5	873	2 Q42595	Q42595 xenopus lae
34	1167.5	24.3	845	1 AD09 MOUSE	Q61072 mus musculus
35	1076	22.4	919	2 Q28659	Q28659 oryctolagus
36	1047.5	21.8	792	2 Q19061	Q19061 saguinus oe
37	1045	21.8	812	2 Q77779	Q77779 bos taurus
38	1033.5	21.5	825	2 Q28477	Q28477 macaca fasc
39	1031.5	21.5	791	1 AD1A MOUSE	Q60813 mus musculus
40	1026.5	21.4	789	1 AD01 RAT	P70505 rattus norv
41	1022.5	21.3	905	2 Q28476	Q28476 macaca fasc
42	1019.5	21.3	825	2 Q46652	Q46652 papio anubi
43	1016	21.2	821	2 Q19060	Q19060 saguinus oe
44	1014.5	21.2	838	2 Q19056	Q19056 papio anubi
45	1007	21.0	804	2 Q60410	Q60410 cavia porce

ALIGNMENTS

RESULT 1

AD02_HUMAN STANDARD; PRT; 735 AA.

AC Q99965; P78326; Q9UCQ8;

DT 30-MAY-2000 (Rel. 39, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)

DE (Fertilin beta subunit) (PH-30) (PH30).

GN Names=ADAM2; Synonyms=FTNB;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;

RX MEDLINE=97193554; PubMed=9041139;

RA Vidaleus C.M., von Kap-Herr C., Golden W.L., Eddy R.L., Shows T.B.,

RA Herr J.C.;

RT "Human fertilin beta: identification, characterization, and

RT chromosomal mapping of an ADAM gene family member.";

RL Mol. Reprod. Dev. 46:363-369(1997).

[2]

RN SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;

RX MEDLINE=96295488; PubMed=8702389;

RA Gupta S.K., Alves K., Palladino L.O., Mark G.E., Hollis G.F.;

RT "Molecular cloning of the human fertilin beta subunit.";

RL Biochem. Biophys. Res. Commun. 224:318-326(1996).

[3]

RN SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;

RX MEDLINE=9724507; PubMed=9070941;

RA Burkin H.R., Burkin D.J., Davey P.M., Griffin D.K., Affara N.A.;

RT "Mapping, sequence, and expression analysis of the human fertilin beta

RT gene (FTNB).";

RL Genomics 40:190-192(1997).

[4]

RN SEQUENCE FROM N.A. (ISOFORM 1).

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;
RT Hall L., Frayne J.;
RA "Nucleotide sequence of the human fertilin beta transcript.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Testis;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Fellings P.S., Wagner L., Schenck C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schenck C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boak S.A., McWeney P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzhanovskiy M.I., Skalska U., Smal M.A.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Sperm surface membrane protein that may be involved in
sperm-egg plasma membrane adhesion and fusion during
fertilization. Could have a direct role in sperm-zona binding or
migration of sperm from the uterus into the oviduct. Interactions
with egg membrane could be mediated via binding between its
disintegrin-like domain to one or more integrins receptors on the
egg. This is a non catalytic metalloprotease-like protein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC -1- Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId-Q99965-1; Sequence=Displayed;
CC Name=2;
CC IsoId-Q99965-2; Sequence=VSP_005471;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expressed specifically in spermatogenic cells
in the seminiferous cells. Not detected in fetal tissues.
CC -1- DOMAIN: A tripeptide motif (PEE) within disintegrin-like domain
could be involved in the binding to egg integrin receptor and thus
could mediate sperm/egg binding.
CC -1- PTM: The prodomain and the metalloprotease domain are cleaved
during the epididymal maturation of the spermatozoa.
CC -1- MISCELLANEOUS: In mammals, exists as a heterodimer composed of an
alpha and beta subunits. In human, fertilin alpha is a pseudogene.
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.ebi.ac.uk/ebis/sequence/>
or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: U52370; AAC51110.1; --
CC EMBL: U38805; AAD04206.1; --
CC EMBL: X99374; CAA67753.1; --
CC EMBL: AJ133005; CAB40813.1; --
CC EMBL: BC034957; AAH34957.1; --
CC PIR: JC4861; JC4861.
CC HSP: P30403; IN4Y.
CC MEROPS: M12.950; --
CC Genew; HGNC:198; ADAM2.

DR MIM; 601533; --
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005178; F: integrin binding; TAS.
DR GO; GO:0008337; F: metalloproteinase activity; TAS.
DR GO; GO:0007342; P: fusion of sperm to egg plasma membrane; TAS.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR002870; Peptidase M12B_N.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep M12B proper; 1.
DR Pfam; PF01421; Repolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR PRINTS; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE NEG.
DR PROSITE; PS01186; EGF_2; FALSE NEG.
KW Alternative splicing; Cell adhesion; EGF-like domain; Glycoprotein;
KW Signal; Transmembrane.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 174
FT CHAIN 175 735 ADAM 2.
FT DOMAIN 175 686 Extracellular (Potential).
FT TRANSMEM 687 707 Potential.
FT DOMAIN 708 735 Cytoplasmic (Potential).
FT DOMAIN 175 382 Metalloprotease-like.
FT DOMAIN 383 475 Disintegrin-like.
FT DOMAIN 477 606 Cys-rich.
FT DOMAIN 612 645 EGF-like.
FT DISULFID 287 370 By similarity.
FT DISULFID 329 354 By similarity.
FT DISULFID 445 458 Potential.
FT DISULFID 616 627 By similarity.
FT DISULFID 621 633 By similarity.
FT DISULFID 635 644 By similarity.
FT CARBOHYD 122 122 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 220 220 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 353 353 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 459 459 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 566 566 N-linked (GLCNAC. .) (Potential).
FT VARSPPLIC 172 190 Missing (in isoform 2).
FT FTID=VSP_005471.
FT CONFLICT 3 3 Missing (in Ref. 2).
FT CONFLICT 21 21 D -> H (in Ref. 3).
FT CONFLICT 99 99 E -> D (in Ref. 3).
FT CONFLICT 106 106 V -> G (in Ref. 3).
FT CONFLICT 170 170 V -> A (in Ref. 2).
FT CONFLICT 288 288 D -> H (in Ref. 1).
FT CONFLICT 321 321 I -> T (in Ref. 1).
FT CONFLICT 388 388 G -> S (in Ref. 3).
FT CONFLICT 396 398 EEC -> DEF (in Ref. 3).
FT CONFLICT 501 501 G -> S (in Ref. 3).
FT CONFLICT 529 529 D -> Y (in Ref. 3).
FT CONFLICT 579 579 S -> G (in Ref. 3).
FT CONFLICT 588 588 W -> L (in Ref. 3).
FT CONFLICT 603 603 N -> D (in Ref. 3).
FT CONFLICT 629 630 NK -> KQ (in Ref. 3).
FT CONFLICT 638 638 S -> F (in Ref. 3).
SQ SEQUENCE 735 AA; 82456 MW; 92867B5340BEE01F CRC64;
Alignment Scores:
Pred. No.: 1,18e-291 Length: 735
Score: 3969.50 Matches: 733
Percent Similarity: 99.73% Conservatives: 0
Best Local Similarity: 99.73% Mismatches: 1
Query Match: 82.77% Indels: 1
DB: 1

US-10-054-683-18 (1-2640) x AD02_HUMAN (1-735)

72 ATGTGG---GTCCTGTTCTGCTCAGCGGGCTCGGGGGCTGGCGATGGACAGTAATTTT 128
Db MetTrpArgValLeuPheLeuLeuSerGlyLeuGlyLeuArgMetAspSerAsnProPhe 20

129 GATAGTTTACCTGTGCAAAATTACAGTTCCGAGAAAATACGGTCAATAATAAAGGAAGGA 188
Db AspSerLeuProValGlnIleThrValProGluLeuIleArgSerIleIleGlyGly 40

189 ATTGAATCGCAGCATCTCAAAATGTAAATTGAAGGGAACCATATACTGTGAATTTA 248
Db IleGluSerGlnAlaSerTyrIleValIleGluGlyProTyrThrValAsnLeu 60

249 ATCAAAAACCTTTTACCCCATAAATTTAGAGTTTACAGTTATAGTGGCACAGGAAT 308
Db MetGlnIleAsnPheLeuProHisAsnPheArgValTyrSerTyrSerGlyThrGlyIle 80

309 ATGAAACCACTTGACCAAGATTTTCAAGATTTCTGCCACTACCAAGGTATATTGAAGGT 368
Db MetLysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGly 100

369 TATCCAAATCTGTGTGATGTTAGCACATGTACTGGACTCAGGGCGTACTACAGTTT 428
Db TyrProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPhe 120

429 GAAAAATGTTAGTTATGAATAGAACCCCTCGAGTCTTCAGTTGGCTTTGAACATGTAAT 488
Db GluAsnValSerTyrGlyIleGluProLeuGluSerValGlyPheGluHisValIle 140

489 TACCAAGTAAACATAAGAAAGCAGATGTTTCTTATATATAGAGAGATATTGAATCA 548
Db TyrGlnValLysHisLysLysAlaAspValSerLeuTyrAsnGluLysAspIleGluSer 160

549 AGAGATCTGCTCTTAAATTACAAAGCGCAGCCACAGCAAGATTTGCAAAATATATA 608
Db ArgAspLeuSerPheLysLeuGlnSerValGluProGlnAspPheAlaTyrIle 180

609 GAAATGATGTTAGTTGAAACCAATTTGTAATCATATGGTCTGTATACAACTGTT 668
Db GluMetHisValIleValGluLysGlnLeuTyrAsnHisMetGlySerAspThrThrVal 200

669 GTCGCTCAAAAGTTTCCAGTTGATTGGAATGACGAATGCTATTTTGTTCATTAAAT 728
Db ValAlaGlnLysValPheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAsn 220

729 ATTACAAATATTCTGCTCTTCAATGGAGCTTGGATAGATGAAATATAAATGGCAACCT 788
Db IleThrIleLeuSerSerLeuGluLeuTrpIleAspGluAsnLysIleAlaThrThr 240

789 GGAGAGCTAATGAGTTATTACACATTTTAAAGATGGAACACATCTTATCTGTTTAA 848
Db GlyGluAlaAsnGluLeuLeuHisThrPheLeuArgTrpLysThrSerTyrLeuValLeu 260

849 CGTCTCATATGCTGGCATTTTACTGTTTACAGAAAAGTCAAAATATTGTTGTGCA 908
Db ArgProHisAspValAlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAla 280

909 ACCTTTCAAGGAGATGTGTGATGCAAACTATGACGAGGTTGTTGTCACCCGAGA 968
Db ThrPheGlnGlyLysMetCysAspAlaAsnTyrAlaGlyValValLeuHisProArg 300

969 ACCATAGCTGGAATCACCTGAGTTATTTAGCTCAATATTAGCCCTTAGTATGGGG 1028
Db ThrIleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGly 320

1029 ATCACTTATGATGACATTAAACATGCGAGTGTCTCAGAGCTGTCTCATTTATGAATCCA 1088
Db IleThrTyrAspAspIleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnPro 340

1089 GAAGCAATTCATTTCAGTGGTGAAGATCTTTAGTAACTGCGAGCTTCGAAGACTTTGCA 1148
Db ValLeuIleAlaIleMetValLysValAsnPheGlnArgLysLysTrpArgThrGluAsp 720

341 GluAlaIleHisPheSerGlyValLysIlePheSerAsnCysSerPheGluAspPheAla 360

1149 CATTTTATTTCAAAGCAGAAAGTCCCAAGTGTCTTTACAATCAGCTCGCTTAGACTCTTTT 1208
Db HisPheIleSerLysGlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPhe 380

1209 TTCAAACAGCAGCAGTGTGTGTAATGCMAAGCTGGAAGCAGGAGAGGAGTGTGACTGT 1268
Db PheLysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluGluCysAspCys 400

1269 GGGACTGAACAGGATTTGCCCTTATTGGAGAAACATGCTGTGATATTGGCACATGTPAGA 1328
Db GlyThrGluGlnAspCysAlaLeuIleGlyLeuThrCysCysAspIleAlaThrCysArg 420

1329 TTTTAAAGCCGGTTTCAAACCTGTCTGAAGGACCACTATGTCGGAACACTGTCTTATTATGTCA 1388
Db PheLysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSer 440

1389 AAAGAAAGAAATGTGTAGGCTTCCCTTTGAAGATGGACCTCCCTCCTGNAATATTGCAATGGA 1448
Db LysGluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGly 460

1449 TCATCTGCATCATGCCCCAGAAAACCACTATGTTTCAGACTGGGCATCCGCTGGACTCAAT 1508
Db SerSerAlaSerCysProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsn 480

1509 CAATGATCTGTATAGATGGAGTTTGTATGAGTGGGATAAAACAATGTACAGACACATTT 1568
Db GlnTrpIleCysIleAspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPhe 500

1569 GGCAAAGAGATAGAGTTTGGCCTTCAGAAATGTTTATCTCACCTTAATTTCAAAGACTGAT 1628
Db GlyLysGluValGluPheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAsp 520

1629 GTATCTGGAACCTGCTATTAAGTAACTAGGATACACAGAGTGAAGCTGCAATCTG 1688
Db ValSerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeu 540

1689 CAGTGGGAAAAATTAATATATGATAGGTAAATTTTTTATACAAATTTCCAAGAGCC 1748
Db GlnCysGlyLysLeuIleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAla 560

1749 ACTATTATTTATGCCAAACATAAGTGACATCTCTGCATTCCTGTGGAATTTGCCAGTGAT 1808
Db ThrIleIleTyrAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAsp 580

1809 CATGCACAGACCCAAAGATGTGATAAAGATGGAACCTCTTGTGTTGTTCAATAAGCTT 1868
Db HisAlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysVal 600

1869 TGCAAGAAATCAAAGATGTGTGAGTTCTTCTATCTTGGGTTATGATTGTACTACTGACAAA 1928
Db CysArgAsnGlnArgCysValSerSerSerTyrLeuGlyTyrAspCysThrThrAspLys 620

1929 TGCAATGATAGAGTGTATGCAATAACAAAGACACTGTCTGCTAGTGTCTTCATATTTA 1988
Db CysAsnAspArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeu 640

1989 CCTCCAGATTGCTCAGTTCATTCAGATCTATGCGCTGCTGGAGTATTGACAGTGGCAAT 2048
Db ProProAspCysSerValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAsn 660

2049 TTTTCCACCTGTAGCTATACCAGCCAGACTCCCTCGAAAGCGCTACATTGAGAACATTATAC 2108
Db PheProProValAlaIleProAlaArgLeuProGluArgArgTyrIleGluAsnIleTyr 680

2109 CATTCCAAACCAATGAGATGGCCATTTTCTTATTCATTCTTCTTTTATTTTCTGT 2168
Db HisSerLysProMetArgTrpProPhePheLeuPheIleProPhePheIleIlePheCys 700

2169 GTACTGATGCTATATGTTGAAAGTTAATTTCCAAAGGAAAGAAATGAGNACTGAGGAC 2228
Db ValLeuIleAlaIleMetValLysValAsnPheGlnArgLysLysTrpArgThrGluAsp 720

QY 2229 TATTCAAGCGATGACCACTGAAAGTGGAGTGAACCTAAAGGG 2273
 Db |||||
 721 TyrSerSerAspGluInProGluSerGluSerGluProLysGly 735

RESULT 2
 AD02_MACFA STANDARD; PRT; 735 AA.
 AC 28478; Q28472;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
 DN (Fertilin beta subunit) (PH-30) (PH30-beta).
 GN Name=ADAM2; Synonyms=FTNB;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=95260313; PubMed=7741716;
 RA Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
 RT "Cloning and analysis of monkey fertilin reveals novel alpha subunit
 isoforms.";
 RL Biochem. J. 307:843-850(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96341733; PubMed=8720115;
 RA Ramarao C.S., Myles D.G., White J.M., Primakoff P.;
 RT "Initial evaluation of fertilin as an immunoreceptive antigen and
 molecular cloning of the cynomolgus monkey fertilin beta subunit.";
 RL Mol. Reprod. Dev. 43:70-75(1996).
 CC -1- FUNCTION: Sperm surface membrane protein that may be involved in
 sperm-egg plasma membrane adhesion and fusion during
 fertilization. Could have a direct role in sperm-zona binding or
 migration of sperm from the uterus into the oviduct. Interactions
 with egg membrane could be mediated via binding between its
 disintegrin-like domain to one or more integrins receptors on the
 egg. This is a non catalytic metalloprotease-like protein (By
 similarity).
 CC -1- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed specifically in testis.
 CC -1- DOMAIN: A tripeptide motif (PDE) within disintegrin-like domain
 could be involved in the binding to egg integrin receptor and thus
 could mediate sperm/egg binding (By similarity).
 CC -1- PTM: The signal and the metalloprotease domain are cleaved during
 the epididymal maturation of the spermatozoa (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.

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 or send an email to license@isb-sib.ch).

 EMBL; X77653; CAAS4733.1; -;
 DR EMBL; U33959; BAB52699.1; -;
 DR PIR; G02937; G02937.
 DR HSP; P30403; IN4Y.
 DR MEROPS; M12.950; -;
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001590; Peptidase_M12B.

DR InterPro; IPR002870; Peptidase_M12B_N.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_Propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR PRODOM; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS00215; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS00214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE NEG.
 DR PROSITE; PS01186; EGF_2; FALSE NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1
 FT PROPEP 17 174 By similarity.
 FT CHAIN 175 735 ADAM 2.
 FT DOMAIN 17 686 Extracellular (Potential).
 FT TRANSMEM 687 707 Potential.
 FT DOMAIN 708 735 Cytoplasmic (Potential).
 FT DOMAIN 175 382 Metalloprotease-like.
 FT DOMAIN 383 475 Disintegrin-like.
 FT DOMAIN 476 606 Cys-rich.
 FT DOMAIN 612 645 EGF-like.
 FT DISULFID 370 370 By similarity.
 FT DISULFID 329 354 By similarity.
 FT DISULFID 445 458 Potential.
 FT DISULFID 616 627 By similarity.
 FT DISULFID 621 633 By similarity.
 FT DISULFID 635 644 By similarity.
 FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 459 459 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 566 566 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 723 723 S -> T (in Ref. 2).
 SQ SEQUENCE 735 AA; 82357 MW; BE84BE115E1D0B53 CRC64;

Alignment Scores:
 Pred. No.: 1.53e-270 Length: 735
 Score: 3690.50 Matches: 672
 Percent Similarity: 95.51% Conservative: 30
 Best Local Similarity: 91.43% Mismatches: 32
 Query Match: 76.95% Indels: 1
 DB: 1 Gaps: 1

US-10-054-683-18 (1-2640) x AD02_MACFA (1-735)

QY 72 ATGTGG---GTCTTGTCTTCTCAGCGGGCTCGCGGGCTGGGATGGACAGTAATTTT 128
 Db |||||
 1 MetTrpArgValLeuPheLeuSerGlyLeuGlyLeuTrpMetAspSerAsnPhe 20

QY 129 GATGATTTACCTGTGCAAAATTACAGTTCGGGAGAAATACGGTCAATAATAAGGAGGA 188
 Db |||||
 21 AspSerLeuProValGlnIleThrValProGluLysIleArgSerIleLeuGluGlu 40

QY 189 ATTGAATCGAGGCATCCTACAAAATTGTAATTGAAGGGAAACCATATATCTGTGAATTTA 248
 Db |||||
 41 IleGluSerGlnValSerTyrLysIleValIleGluGlyLysProTyrThrAlaAsnLeu 60

QY 249 ATGCAAAAAAATTTTACCCTAATTTTACAGTTTACAGTTTACAGTTTACAGTTTACAGTTT 308
 Db |||||
 61 MetGlnLysAsnPheLeuSerHisAsnPheArgValTyrSerTyrAsnGlyThrGlyIle 80

QY 309 ATGAAACCACTTGACCAAGATTTTCCAGAAATTTTCCAGAAATTTTCCAGAAATTTTCCAGAA 368
 Db |||||
 81 MetLysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGly 100

QY 369 TATCCAAAATCTGT 428
 Db |||||
 101 TyrProLysSerValAlaMetValSerThrCysThrGlyLeuArgGlyLeuLeuGlnPhe 120


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QY 429 GAAAAAGTTAGTTATGAATAGAACCCCTCGAGTCTTTCAGTTGGCTTTGAAACATGTAATT 488
Db 121 GluAsnValSerTyrGlyIleGluProLeuGluSerValGlyPheGluHisValIle 140
QY 489 TACCAAGTAAACATAGAAGCAGAGTGTTCCTTATATATATAGAGAGGATATTGAAATCA 548
Db 141 TyrGlnValIleHisValAlaAspValSerLeuTyrAsnGluIleGluSer 160
QY 549 AGAGATCTGCTCTTAAATATACAAAGCGCAGAGCCACAGCAAGATTTTGCAAAAGTATATA 608
Db 161 ArgAspLeuSerPheIleGlnSerIleGluProGlnIleHisPheAlaIleTyrIle 180
QY 609 GAAATGATGTTATAGTTGAAAACAAATGTTATATATATAGAGGCTCTGATACAACTGTT 668
Db 181 GluMetHisValValGluIleGlnLeuTyrAsnHisMetGlySerGlyThrThrVal 200
QY 669 GTCGCTCAAAAGCTTTTCCAGTTGATTGGAATGCAGCAATGCTATTTTGTTCATTATAT 728
Db 201 ValThrGlnIleHisPheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerLeuAsn 220
QY 729 ATTACAAATATTCTGCTCTTCATTGGAGCTTTGGATAGATGAAATATAAATTCGAACCACT 788
Db 221 IleThrValIleLeuSerSerLeuGluLeuTyrIleAspGluAsnIleAlaThrThr 240
QY 789 GGAGAAGCTAATGAGTTATTACACACATTTTAAAGATGGAAACATCTTATCTGTTTAA 848
Db 241 GlyAspAlaIleGluLeuHisThrPheLeuArgTyrIleArgSerTyrLeuValLeu 260
QY 849 CGTCCTCATGATCGGCATTTTACTGTTTGTACAGAAAGTCAAAATATGTTGGTGA 908
Db 261 ArgProHisAspValAlaPheLeuLeuValTyrArgGluIleSerAsnTyrValGlyAla 280
QY 909 ACCTTTCAAGGAGAGTGTGTGATGCAAACTATGACAGGAGTGTGTTCTGCAACCCAGA 968
Db 281 ThrPheGlnGlyIleMetCysAspAlaAsnTyrAlaGlyValLeuLeuHisProArg 300
QY 969 ACCATAGTCTGAAATCATTGAGTATTTTAACTCAATATATAGCCCTTAGTATGGGG 1028
Db 301 ThrIleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGly 320
QY 1029 ATCAGTATGATGATCAATTAACAAATCCAGTGTCTCAGGAGCTCTGCAATATGATATCA 1088
Db 321 IleProTyrAspAspIleAsnGlnCysGlnCysSerAlaAlaValCysIleMetAsnPro 340
QY 1089 GAAGCAATTCATTTCAGTGTGTGAAGATCTTTAGTAACTGCAGCTTCGAAGACTTTGCA 1148
Db 341 GluAlaIleHisPheSerGlyValIlePheSerAsnCysSerIleGluAspPheAla 360
QY 1149 CATTATTTCAAAGCAGAGTCCCAAGTGTCTTCAATCAGCCTCGCTTAGATCTCTTT 1208
Db 361 HisPheIleSerIleGlnIleSerGlnCysLeuHisAsnGlnProArgLeuAspProPhe 380
QY 1209 TTCAACAGCAGCAGTGTGTGATGCAAACTGCAAGCTGCAAGCAGGAGGAGTGTGACTGT 1268
Db 381 PheIleGlnGlnAlaValCysGlyAsnAlaIleLeuGluAlaGlyGluGluCysAspCys 400
QY 1269 GGAGCTGAACAGGATGTGGCTTTATGGAGAAACATGCTGTGATATTGGCAGATGAGA 1328
Db 401 GlyThrGlnGlnAsnCysPheLeuLeuGlyAlaIleCysCysAspThrAlaThrCysArg 420
QY 1329 TTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGCTGCGAAAACATGCTCTATTATGTCA 1388
Db 421 PheIleAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSer 440
QY 1389 AAAGAAAGATGTAGGCTCTCTTTGAAGATGCGACCTCCCTGAAATATTCGAATGGA 1448
Db 441 GlnGluArgValCysArgProSerPheAspGluCysAspLeuProGluTyrCysAsnGly 460
QY 1449 TCATCTGCATCATGCCAGAAAACCACTATGTTTCAGACTGGGCATCCGTGTGACTGAAT 1508
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QY 1509 CAATGATCTGTATAGATGAGTGTGTATGATGAGTGGGATAAACAATGTACAGACACATTT 1568
Db 481 GlnTrpValCysIleAspGlyValCysMetAsnGlyAspIleGlnCysMetAspThrPhe 500
QY 1569 GGCAAAAGAGTACAGTTTGGCCCTTCAGAAATGTTTATTCACCTTAATTCAAAGACTGAT 1628
Db 501 GlyGluGluAlaGluPheGlyProThrGluCysTyrSerTyrLeuAsnSerIleThrAsp 520
QY 1629 GTATCTGGAAACTGTGTATAGTGTATAGGATACACAGTGTGAAAGTGCACAACTGT 1688
Db 521 ValSerGlyAsnCysGlyIleGlyAspSerGlyTyrThrGlnCysGluAlaAspAsnLeu 540
QY 1689 CAGTGGCGAAAATAATATATGTAATATAGTAGGTAAATTTTATACAAATTCGAAGGCC 1748
Db 541 GlnCysGlyIleLeuIleCysIleTyrAlaGlyGluPheLeuLeuGlnIleProArgAla 560
QY 1749 ACTATTATTATGCCCAACATAAGTGCACATCTCTGCATTGCTGTGAAATTTGCCAGTAT 1808
Db 561 ThrIleIleTyrAlaAsnIleSerGlyHisLeuCysValAlaValGluPheAlaSerAsp 580
QY 1809 CATCCAGACAGCCAAAAGATGTGGATAAAGATGGAACCTTCTTGTGGTTCAATAAGGTT 1868
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QY 1869 TGCAAGAAATCAAGATGTGTGAGTCTTCTCATCTACTGCTGGTATGATGTACTACTGACAA 1928
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QY 1929 TGCAATGATAGAGTGTGTGCAATAACAAAACACTGTCTCAGTGTAGTGTCTATATTTA 1988
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QY 1989 CTCCAGATTTGCTCAGTTCAATCAGATCTATGCGCTGGTGGAGTATTGACAGTGGCAAT 2048
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QY 2049 TTTCCAGCTGTAGCTATACAGCCACACTCCCTGAAAGCGCTACATTGAGAACATTTAC 2108
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QY 2109 CATTCCAAACCAATGAGATGGCCATTTTCTTATTCATTCTCTTCTTATTTCTTCTGT 2168
Db 681 HisSerIleProMetArgIrrProLeuPheLeuPheIleProPheIleIlePheCys 700
QY 2169 GTACTGATGCTATAATGTTGAAGTTAAATTTCCAAAGGAAAAAATGGAGAACTGGAGC 2228
Db 701 ValIleIleAlaIleMetValIleValHisPheGlnArgIleYsIrrArgThrGluAsp 720
QY 2229 TATTCAAGCGATGAGCAACTGAAAGTGAAGTGAACCTTAACGGG 2273
Db 721 TyrSerAspGluGlnProGluSerGluSerGluProIleGly 735
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ID Q6P2G0
AC Q6P2G0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ADAM2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC064547; AAH64547.1; -
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propag; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PD00289; DISINTEGRIN.
DR PRODOM; PD00664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
SQ SEQUENCE 579 AA; 64795 MW; 1F7AF0CDA2A064F9 CRC64;

Alignment Scores:
Pred. No.: 2,97e-233 Length: 579
Score: 3065.50 Matches: 577
Percent Similarity: 78.50% Conservative: 0
Best Local Similarity: 78.50% Mismatches: 1
Query Match: 63.92% Indels: 157
DB: 2 Gaps: 3

US-10-054-683-18 (1-2640) x Q6P2G0 (1-579)

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DB 1 MetTrpArgValLeuPheLeuLeuSerGlyLeuGlyGlyLeuArgMetAspSerAsnPhe 20

QY 129 GATAGTTTACTGTGCAAAATACAGTCCGAGAGAAATACGGTCAATAATAAGGAAGGA 188
DB 21 AspSerLeuProValGlnIleThrValProGluLysIleArgSerIleLeuLysGluGly 40

QY 189 ATTCAATCGCAGGCATCTCAAAAATGTAAATGAAGGAAACCATATCTGTGAATTTA 248
DB 41 IleGluSerGlnAlaSerTyrLysIleValIleGluLysProTyrThrValAsnLeu 60

QY 249 ATGCAAAAACTTTTACCCCAATAATTTAGAGTTTACAGTTATAGTGGCAGAGGAATT 308
DB 61 MetGlnLysAsnPheLeuProHiaAsnPheArgValTyrSerTyrSerGlyThrGlyLe 80

QY 309 ATGAACACCTTGACCAAGATTTTCAGAAATTTCTGCCACTACCAAGGTATATTGAAGGT 368
DB 81 MetLysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGly 100

QY 369 TATCCAAAATCTGGTGTATGGTATGACATCTACTTGGACTCAGGGCGGTACTACAGTTT 428
DB 101 TyrProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPhe 120

QY 429 GAAATGTTAGTTATGGAATAGAACCCCTCGAGTCTTCAGTTCGCTTGAACATGTAATT 488

DB 121 GluAsnValSerTyrGlyIleGluProLeuGluSerSerValGlyPheGluHisValIle 140
QY 489 TACCAAGTAAAAACATAAGAACGACAGATGTTCTTATATATAATGAGAAGGATATTGAATCA 548
DB 141 TyrGlnValLysHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 160
QY 549 AGAGATCTGTCTCTTTAAATTTACAAAGCGCAGAGCCACAGCAAGATTTTCCAAAGTATATA 608
DB 161 ArgAspLeuSerPheLysLeuGlnSerValGlu----- 171
QY 609 GAAATGCATGTTATAGTTGAAAAACAATTTGTATATATCATATGGGGCTGATACAACTGTT 668
DB 171 ----- 171
QY 669 GTCGCTCAAAAAGTTTTCAGTGTGATTGGATTGACGAATGCTATTTTCTTTCATTAAAT 728
DB 171 ----- 171
QY 729 ATTACAAATTTCTGCTTCTTCTGATGGAGCTTTGGATAGATGAATAATAATTCGAACCACT 788
DB 171 ----- 171
QY 789 GGAGAAGCTAATGAGTTATTACACACATTTTAAAGATGGAAAACATCTTATCTTGTGTTTA 848
DB 171 ----- 171
QY 849 CGTCCTCATGATGTGGCATTCTTCTGTTTACAGAGAAAAAGTCAAAATTTATGTTGGTGCA 908
DB 171 ----- 171
QY 909 ACCTTTCAAGGGAAGATGTGTGATGCAAACTATGCAAGAGGTTGTTCTGTCGACCCACAGA 968
DB 172 -----HisProArg 174

QY 969 ACCATAAGTCTGGAATCACTTCAGTTATTTTAGCTCAATATTAGTGCCTTAGTATGGGG 1028
DB 175 ThrIleSerLeuGlnSerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGly 194

QY 1029 ATCACTTATGATGACATTAACAAATGCCAGTGTCTCAGGAGCTGTCTGCAATATGAAATCCA 1088
DB 195 IleThrTyrAspAspIleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnPro 214

QY 1089 GAAGCAATTCATTTTCAGTGTGTAAGATCTTTAGTAACTGCGAGCTTCAAGAGCTTTGCA 1148
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QY 1149 CATTTTATTTCAAGCAGAGTCCCAAGTGTCTTCAATCAGCTCGCTTAGATCCCTTTT 1208
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QY 1209 TTTCAAAACAGCAAGCAGTGTGTGTAATGCAAAAGCTGGAAGCAGAGAGAGTGTGACTGT 1268
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QY 1329 TTTTAAAGCCGTTTCAAACTGTGCTGAAGGACCATGCTGCGAAAATCTGTCTTATTATGTCA 1388
DB 295 PheLysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSer 314

QY 1389 AAAGAAGAATGTGTAGGCTCTCTTTGAAGAAGTGGACCTCCCTCGAATATTCGAATGGA 1448
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QY 1509 CAATGGATCTGTATAGATGAGTGTGTATGAGTGGGATGAACAATGTACAGACATTT 1568
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QY 1569 GCAAGAAAGTAGAGTTGGCCCTTCAGAAATGTTATTCACCTTAATTCACAAAGACTGAT 1628
 DB 375 GlyLeuValGluPheGlyProSerGluCysTy-SerHisLeuAenSerLysThrAep 394
 QY 1629 GTATCTGGAACATGCTGATTAAGTATTCAGGATACACACAGTGTGAAGCTGCAATCTG 1688
 DB 395 ValSerGlyAenCysGlyHisSerAepSerGlyTyThrGlnCysGluAlaAep----- 412
 QY 1689 CAGTGGGAAATTAATATGTAATATGAGTAAATTTTATTACAAATTCACAGAGCC 1748
 DB 412 ----- 412
 QY 1749 ACTATTATTATGCCAACATAAGTGGACATCTCTGCATTCCTGTGGAATTTGCCAGTGAT 1808
 DB 413 -----GlyHisLeuCysAlaValGluPheAlaSerAep 424
 QY 1809 CATGCACAGACCCAAAAGATGTGGATAAAGATGGAACCTCTTGTGGTTCAAATAAGTT 1868
 DB 425 HisAlaAepSerGlnLysMetTrpIleLysAepGlyThrSerCysGlySerAenLysVal 444
 QY 1869 TGCAGGAATCAAGATGTGTGAGTCTTCTCATCTTGGTTATGATGTACTACTGACAAA 1928
 DB 445 CysArgAenGlnArgCysValSerSerTyLeuGlyTyArgCysThrThrAepLys 464
 QY 1929 TGCATGATAGAGGTGTATGCAATAACAAAGACACTGTCACTGTAGTGTCTCATATTTA 1988
 DB 465 CysAenAepArgGlyValCysAenAenLysHisCysHisCysSerAlaSerTyLeu 484
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 QY 2049 TTTCCACCTGTAGCTATPACAGCCAGACTCCCTGAAAGCGCTACATTGAGAACATTAC 2108
 DB 505 PheProValAlaIleProAlaAe-gleuProGluArgTyIleGluAenIleTy 524
 QY 2109 CATTCACAAACATAGATGGCCATTTTCTTATTCATCTCTTCTTATTTATTTCTGT 2168
 DB 525 HisSerLysProMetArgTrpProPhePheLeuPheIleProPheIleIlePheCys 544
 QY 2169 GTACTGATCTCTAATGTGGAAGTAAATTCACAAAGGAAAAATTCGAGAACTGAGGAC 2228
 DB 545 ValLeuIleAlaIleMetValLysValAenPheGlnArgLysLysTrpArgThrGluAep 564
 QY 2229 TATTCAAGCATGAGCAACCTGAAAGTGAGAGTGAACCTAAAGG 2273
 DB 565 Ty-SerSerAepGluGlnProGluSerGluSerGluProLysGly 579

RESULT 4
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 AC AAH64547;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE ADAM2 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC064547; AAH64547.1; -. 1F7AP0CDA2A064F9 CRC64;
 SQ SEQUENCE 579 AA; 64795 MW; 1F7AP0CDA2A064F9 CRC64;

Alignment Scores:

Pred. No.: 2,97e-223 Length: 579
 Score: 3065.50 Matches: 577
 Percent Similarity: 78.50% Conservative: 0
 Best Local Similarity: 78.50% Mismatches: 1
 Query Match: 63.92% Indels: 157
 DB: 2 Gaps: 3

US-10-054-683-18 (1-2640) x AAH64547 (1-579)

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 QY 129 GATAGTTTACCTGTGCAATTCAGTTCGAGAAAATACGTCATTAATAAAGGAGGA 188
 DB 21 AspSerLeuProValGlnIleThrValProGluLysIleArgSerIleLysGluGly 40
 QY 189 ATTGAATCGAGCATCTACAAAATTGTAATTAAGGGGAAACATATACCTGTGAATTTA 248
 DB 41 IleGluSerGlnAlaSerTyIleValIleGluGlyLysProTyThrValAenLeu 60
 QY 249 ATGCAAAAAAATTTTACCCATAATTTTACAGTTTACAGTTTATAGTGCACAGGAAT 308
 DB 61 MetGlnLysAenPheLeuProHisAenPheArgValTy-SerTySerGlyThrGlyLe 80
 QY 309 ATGAAACCACTTCACCAAGATTTTCAGATTTTCGCACCTACCAAGGCTATATGAAGT 368
 DB 81 MetLysProLeuAepGlnAepPheGlnAenPheCysHisTyIleGluGly 100
 QY 369 TATCCAAAATCTGT 428
 DB 101 TyrProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPhe 120
 QY 429 GAAAAATGTTAGTTATGGAATAGAACCCCTGGAGTCTTTCAGTTCGCTTTGAACATGTAAT 488
 DB 121 GluAenValSerTyIleGluProLeuGluSerSerValGlyPheGluHisValIle 140
 QY 489 TACCAAGTAAACATAGAAAGCAGATGTTTCTTATATATAGAGGATATATGATCA 548
 DB 141 TyGlnValLysHisLysLysAlaAepValSerLeuTyAenGluLysAepIleGluSer 160
 QY 549 AGAGATCTGTCTTTAAATTTACAAAGCGCAGAGCCACAGCAAGATTTTGCAGAGTATATA 608
 DB 161 ArgAepLysSerPheLysLeuGlnSerValGlu----- 171
 QY 609 GAAATGCATGTTATAGTTGAAAAACAAATTTGTATTAATCATATGGGCTGTGATACAACTGTT 668
 DB 171 ----- 171
 QY 669 GTCGCTCAAAAAGCTTTTCCAGTTGATTTGATTCAGCATCTATTTTGTTCATTTAAT 728
 DB 171 ----- 171

QY 729 ATTACAAATTATTCTGCTTCATTTGGAGCTTTGGATAGATGAATAAATAATGCAACCACT 788
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QY 789 GGAGAAGCTAATGAGTTATTACACACATTTTAAAGATGGAAACATCTTATCTTGTGTTTA 848
Db 171 ----- 171
QY 849 CGTCCTCATGATGGCAATTTTACTTGTGTTTACAGAGAAAGCAAAATATGTTGGTGCA 908
Db 171 ----- 171
QY 909 ACCTTTCAAGGGAAGATGTGTGATGCAAACTATGCAGGAGGTGTGTTCTGCAACCCGAGA 968
Db 172 -----HisProArg 174
QY 969 ACCATAAGTCTGGAATCACTTGCAGTTATTATTAGCTCAATATTAGCCCTTAGTATGGG 1028
Db 175 ThrIleSerLeuGluSerLeuAlaValIleLeuAlaGlnLeuLeuSerMetGly 194
QY 1029 ATCACTTATGATGACATTACAAATGCGAGTCTCAGAGCTGTCTGCATATGATATCCA 1088
Db 195 IleThrTyrAspAspIleAenLysCysGlnCysSerGlyAlaValCysIleMetAsnPro 214
QY 1089 GAAGCAATTCATTTCACTGGTGTGAAGATCTTTAGTAACTGACGCTTCGAAGACTTTGCA 1148
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Db 255 PheLysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluCysAspCys 274
QY 1269 GGGAGTCAACAGGATTTGGCCCTTATTGGAGAAACACTGCTGTGATATTGGCACATGAGA 1328
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QY 1329 TTTAAAGCCGGTTCAACTGTGCTGAAGGACCATGCTGCGAAACACTGCTATTATGTCA 1388
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QY 1389 AAAGAAAGAAATGCTAGCCCTTCCTTGAAGATGCGACCTCCCTGATATTTGCAATGGA 1448
Db 315 LysGluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGly 334
QY 1449 TCATCTGCATCATGCCAGAAACCACTATGTTTCAAGTGGGCACTCCGCTGTGGACTGAAT 1508
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QY 1509 CAATGGATCTGTATAGTGGAGTTTGTATAGTGGGGATAAACAAATGTACAGACACATTT 1568
Db 355 GlnTrpIleCysIleAspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPhe 374
QY 1569 GGCAAGAGTAGATTTGGCCCTTCAGATGTTATTCTCACTTAATTCAGAGCTGACAAATCTG 1628
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QY 1629 GTATCTGAAACTGTGGTATAGTATAGTGGGGATAAACAAATGTACAGACACATTT 1688
Db 395 ValSerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAsp----- 412
QY 1689 CAGTCCGGAAATAATATGTAATATGTAATATGTAATATTTTATACAAATTCAGAGGCC 1748
Db 412 ----- 412
QY 1749 ACTATTATTATGCCAACATAGTGCACATCTCTGATTTGCTGGAATTTGCCAGTGTAT 1808
Db 413 -----GlyHisLeuCysIleAlaValGluPheAlaSerAsp 424

QY 1809 CATGCAGACAGCAAAAGATGTGGATAAAGATGGAACCTCTTGTGGTTCAATAGGTT 1868
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QY 1869 TCAGGAATCAAGAGTGTGAGTCTTTCATACTTGGGTATGATTGTACTACTACAAA 1928
Db 445 CysArgAsnGlnArgCysValSerSerSerTyrLeuGlyTyrAspCysThrThrAspLys 464
QY 1929 TCCAATGATAGAGTGTATGCAATAACAAAAAGCACTGTCACTGTAGTGTCTCATATTTA 1988
Db 465 CysAsnAspArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeu 484
QY 1989 CTCCAGATTGCTCAGTTCATCAATCAGATCATGGCCTGTGGAGAGTATTCAGAGTGGCAAT 2048
Db 485 ProProAspCysSerValGlnSerAspLeuTrpProGlyLysIleAspSerGlyAsn 504
QY 2049 TTTCCACCTGTAGCTATACCCAGCCAGCTCCCTGAAAGCGCTACATTCAGAGAACATTAC 2108
Db 505 PheProProValAlaIleProAlaArgLeuProGluArgTyrIleGluAsnIleTyr 524
QY 2109 CATTCCAAACCAATCAGATGGCCATTTTCTTATTTCATTCTCTTATTATTCTCTGT 2168
Db 525 HisSerLysProMetArgTrpPhePheLeuPheIleProPhePheIleIlePheCys 544
QY 2169 GTACTGATTGCTATTAATGTGAAGTTAATTTCCAAAGGAAAAATGGAGAACTGAGGAC 2228
Db 545 ValLeuIleAlaIleMetValLysValAsnPheGlnArgLysLysIleArgTrpArgThrGluAsp 564
QY 2229 TATTCAAGCGATCAGCAACCTGAACTGAGAGTGAACTTAAAGGG 2273
Db 565 TyrSerSerAspGluGlnProGluSerGluSerGluProLysGly 579
RESULT 5
Q866A8 PRELIMINARY; PRT; 735 AA.
ID Q866A8
AC Q866A8
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pertilin beta.
GN Name=PTNB;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22872989; PubMed=14510675;
RA Day A.E., Quilter C.R., Sargent C.A., Mileham A.J.;
RT "Chromosomal mapping, sequence and transcription analysis of the
porcine fertilin beta gene (ADAM2).";
RL Anim. Genet. 34:375-378(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Day A.;
RL Thesis (2004), Department of Applied Sciences, Anglia Polytechnic
University, Cambridge, United Kingdom.
RL EMBL; AJ309003; CAC84225.2; -.
DR HSP; P18619; IPVL.
DR MEROPS; M12.950; -.
DR GO; GO:0004222; F:metallopeptidase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR008994; Nucleic_acid_OR.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.

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CC EMBL; AF086808; AAC62753.1; --
CC DR HSSP; P18619; 1FVL.
CC DR MEROPS; M12.950; --
CC DR InterPro; IPR006586; ADAM cysteine.
CC DR InterPro; IPR001762; Disintegrin.
CC DR InterPro; IPR000742; EGF_2.
CC DR InterPro; IPR006209; EGF_like.
CC DR InterPro; IPR006210; IEGF.
CC DR InterPro; IPR008994; Nucleic acid OB.
CC DR InterPro; IPR001590; Peptidase M12B.
CC DR InterPro; IPR002870; Peptidase M12B_N.
CC DR Pfam; PF00200; Disintegrin; 1.
CC DR Pfam; PF01582; Pep_M12B_propep; 1.
CC DR Pfam; PF01421; Reprolysin; 1.
CC DR PRINTS; PR00289; DISINTEGRIN.
CC DR ProDom; PD000664; Disintegrin; 1.
CC DR SMART; SM00608; ACR; 1.
CC DR SMART; SM00050; DISIN; 1.
CC DR SMART; SM00181; EGF; 1.
CC DR PROSITE; PS00215; ADAM_MBP; 1.
CC DR PROSITE; PS00427; DISINTEGRIN_1; 1.
CC DR PROSITE; PS00214; DISINTEGRIN_2; 1.
CC DR PROSITE; PS00022; EGF_1; FALSE_NEG.
CC DR PROSITE; PS01186; EGF_2; FALSE_NEG.
CC DR PROSITE; PS00026; EGF_3; 1.
CC DR Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
CC KW SIGNAL 1 16 Potential.
CC FT PROPEP 17 174 By similarity.
CC FT CHAIN 175 745 ADAM 2.
CC FT DOMAIN 17 696 Extracellular (Potential).
CC FT TRANSMEM 697 717 Potential.
CC FT DOMAIN 718 745 Cytoplasmic (Potential).
CC FT DOMAIN 175 382 Metalloprotease-like.
CC FT DOMAIN 383 474 Disintegrin-like.
CC FT DOMAIN 475 605 Cys-rich.
CC FT DOMAIN 611 644 EGF-like.
CC FT DOMAIN 148 151 Poly-Ser.
CC FT DISULFID 287 370 By similarity.
CC FT DISULFID 329 354 By similarity.
CC FT DISULFID 444 457 Potential.
CC FT DISULFID 615 626 By similarity.
CC FT DISULFID 620 632 By similarity.
CC FT DISULFID 634 643 By similarity.
CC FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 558 558 N-linked (GlcNAc...) (Potential).
CC SQ SEQUENCE 745 AA; 83150 MW; B5DBDC0168999B00 CRC64;

Alignment Scores:
Pred. No.: 2,51e-197 Length: 745
Score: 2723.00 Matches: 481
Percent Similarity: 78.71% Conservative: 103
Best Local Similarity: 64.82% Mismatches: 146
Query Match: 56.78% Indels: 12
DB: 1 Gaps: 2

US-10-054-683-18 (1-2640) x AD02_BOVIN (1-745)

QY 78 GTCTGTGTTCTGCTCAGCGGGCTCGGGGCTCGGGAGTAAATTTTGTAGTTTA 137
Db 4 LeuLeuPheLeuLeuLeuLeuGlyLeuThrGlyLeuThrAspAspAsnSerGluArgLeu 23
QY 138 CCTGTGCAAAATTACGTTCCGGAGAAATACGTCATATAAAGGAAGGAATTTGAATCG 197
Db 24 ArgValGlnPheThrValProGluLeuIleArgSerThrSerGlyGlyValGluThr 43
QY 198 CAGGCATCCTACAAAATTGTAATTTGAAGGGGAACCATATATCTGTGAATTTTAAATCAAAAA 257

1938 AGAGGTGATGCAATAACAAAAGCACTGTCTACGTAGTGTCTCATATTTTACCTCCAGAT 1997
Db 623 GlnGlyValCysAsnAsnLysArgAsnCysHisCysLysProThrThrLeuProProAsn 642

1998 TGCTCAGTTCAATCAGATCTATGCGCTGGTGGGAGTATTGACAGTGGCAATTTTCCACCT 2057
Db 643 CysGluValSerValGluSerTrpProGlyGlySerValAspSerGlyAsnPheProPro 662

2058 GTAGCTATACCA---GCCAGACTCCTGAAAGGCGCTACATTGAGACATTACCATTC 2114
Db 663 AlaAlaAspProLeuProGlyValProAspArgArgTyrIleGluAsnIleTyrHisSer 682

2115 AAACCAATGAGATGCGCATTTTCTTATTCATTCCTTTCTTTATTTATTTCTGTGTACTG 2174
Db 683 ArgProMetLysTrpProPhePheLeuLeuLeuProPhePheIleLeuCysValLeu 702

2175 ATTGCTATAATGGTGAAGTTAATTTCCAAAGGAAAAATGAGAACTGAGGACTATTCA 2234
Db 703 IleAlaThrLeuValLysIleTyrPheGlnArgLysLysGlyArgThrGluAspAspThr 722

2235 AGCGATGAGCACTGAAAGTGAAGTGAACCTAAA 2270
Db 723 SerAspGlnLeuGluSerGluSerGluThrLys 734

RESULT 6
AD02_BOVIN
ID _AD02_BOVIN STANDARD; PRT; 745 AA.
AC 077780;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
GN Name=ADAM2; Synonyms=FTNB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97304362; PubMed=9160725;
RA Waters S.I., White J.M.;
RT "Biochemical and molecular characterization of bovine fertilin alpha and beta (ADAM 1 and ADAM 2): a candidate sperm-egg binding/fusion complex.";
RL Biol. Reprod. 56:1245-1254 (1997).
CC -1- FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By similarity).
CC -1- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -1- DOMAIN: A tripeptide motif (TDE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).
CC -1- PTM: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -----
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Db 44 HisValSerTyrIleLeuIleGluGlyLysThrTyrValAsnLeuMetGlnLys 63
QY 258 AACTTTTACCCATAATTTAGAGTTTACAGTTATAGTGGCACAGGAATTTATGAACCA 317
Db 64 AlaPheLeuProHisAsnPheArgValTyrGlyTyrSerGlyThrGlySerMetLysPro 83
QY 318 CTTGACACAGATTTTCAGAAATTTCTGCCACTACAAAGGGTATATTGAAGGTTATCAAAA 377
Db 84 LeuGluHisGluPheGlnAsnPheCysTyrTyrGlnGlyTyrIleGluGlyTyrProAsn 103
QY 378 TCTGTGGTGTAGTGTAGCATCTACTGACTCAGGGGCTACTACAGTTTGAATGTT 437
Db 104 SerMetAlaIleIleSerThrCysThrGlyLeuArgGlyLeuLeuGlnPheGluAsnVal 123
QY 438 AGTTATGGAATAGAACCCCTGGAGTCTTCAAGTGGCTTTCAACATGTAATTTACCAAGTA 497
Db 124 SerTyrGlyIleGluProLeuGluProSerIleGlyPheGluHisMetValTyrGlnIle 143
QY 498 AAACATAAGAACAGAGATTTCTTATATATAATGAGAGGATATTGAATCAAGAGATCTG 557
Db 144 LysProArgAspSerSerSerValTyrThrGluArgGluIleGluLeuArgGluLys 163
QY 558 TCCTTTAAATTACAAAGCGCAGAGCCACACAGATTTTCCAAAGTATATAGAAATGCAT 617
Db 164 ProTyrLysIleGlnAsnValGluProLeuProAspPheSerGlnTyrIleGluMetHis 183
QY 618 GTTATAGTTCAAAAACAAATTTGATATATCATATGGGTCTGATACAACTGTGTGCTCAA 677
Db 184 IleValGluLysAspLeuTyrAsnHisMetGlyAlaAspThrThrValValIleGln 203
QY 678 AAAGTTTTCAGTTGATTGACGAATGCTATTTTCTTCAATTAATATATACAAAT 737
Db 204 LysIlePheGlnLeuThrGlyLeuThrAsnAlaIlePheThrSerLeuAsnIleThrVal 223
QY 738 ATTCTGCTTCATTTGAGCTTTGGATAGATAGAAATTAATTAATTCAGGAGAAGCT 797
Db 224 IleLeuSerSerLeuGluLeuTyrIleAspGluAsnLysIleProValThrGlyAspAla 243
QY 798 AATGAGTTATTACACATTTTAAAGATGGAACATCTTATCTTGTTTTACGTCTCAT 857
Db 244 AsnGluLeuLeuHisArgPheValTyrIlePheArgSerTyrLeuValLeuArgProHis 263
QY 858 GATGTGSCATTTTACTTGTATTACAGAGAAAGTCAAAATTTATGTTGTCGAACCTTTCAA 917
Db 264 AspMetAlaPheLeuLeuValTyrArgGluLysSerAsnTyrIleGlyAlaThrPheGln 283
QY 918 GGGAAGATGTGATGCAAACTATGCAAGAGGTGTTGTTCTGCAACCCCAAGACCATAGT 977
Db 284 GlyArgMetCysAspLysHisTyrGlyGlyValAlaLeuHisSerSerThrIleSer 303
QY 978 CTGGAATCCTGTCAGTTATTTAGCTCAATATTAGCCCTTAGTATGGGATCAGCTTAT 1037
Db 304 LeuGluSerLeuAlaValIleIleAlaGlnLeuLeuSerLeuSerMetGlyIleProTyr 323
QY 1038 GATGACATTAACAAATGCCAGTGTCTCAGGAGCTGCTGCAATTTATGAATCCAGAGCAAT 1097
Db 324 AspAspIleAsnLysCysHisCysProGlyAspValCysIleMetAsnProAlaAlaVal 343
QY 1098 CATTTCAGTGGTGAAGATCTTTTAGTAACATGCAAGCTTCGAAGACTTTTGACATTTTATT 1157
Db 344 HisSerSerGlyValLysLeuPhePheSerAsnCysSerValGluAspPheLeuArgPheIle 363
QY 1158 TCAAGCAGAGTCCAGTCTCTCAACATCAGCTCGCTTAGATCTCTTTTTCAAACAG 1217
Db 364 SerLysProLysSerGlnCysLeuGlnAsnGlnProArgLeuAspProThrTyrLys--- 382
QY 1218 CAAGCAGTGTGTGTAATGCAAGCTGCAAGCAGGAGGAGTGTGACTGTGGGACTGAA 1277
Db 383 SerAlaValCysGlyAsnGlyLysValGluGluGlnCysAspCysGlyAsnLys 402
QY 1278 CAGGATTTGCCCTTATTGGAGAAACATGCTGTGATATGCCACATGTAGATTTAAAGCC 1337
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
```

RESULT 7

AD02_RABIT

ID AD02_RABIT STANDARD; PRT; 751 AA.

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Db 403 LysAlaCysAspAlaLeuProAspThrCysCysValAlaAspThrCysArgPheGlnPro 422
QY 1338 GGTCAAACCTGTCTGAGGACCATCTCGAAACCTGTCTATTATGTCAAAGAAGA 1397
Db 423 GlySerAlaCysAspThrGlyLeuCysCysGluSerCysAlaPheIleProLysGlyHis 442
QY 1398 ATGTGTAGGCTTCCCTTTGAAGNATCGGACCTCCCTGAATATTGCAATGATCTGCA 1457
Db 443 IleCysArgGlySerThrAspGluCysAspLeuHisGluTyrCysAsnGlySerSerAla 462
QY 1458 TCATGCCCAAGAAACCACTATTGTCAGACTGGGCATCCGTGTGCACTGAATCAATGATC 1517
Db 463 AlaCysGlnGluAspValTyrValGlnAspGlyHisProCysGlyGlnAsnGlnTyrLeu 482
QY 1518 TGTATAGATGGAGTTTGTATGAGTGGGATAAACAATGTACACACACATTTGGCAAGAA 1577
Db 483 CysIleSerGlyIleCysValAspGlyIleLysGlnCysPheAspIlePheGlyGluGly 502
QY 1578 GTAGATTTGGCCCTTCAGAAATGTTATTCTCACCTTAATTCAAAGACTGATGTATCTGA 1637
Db 503 ThrSerTyrAlaProAlaGluCysPheGlnArgLeuAsnSerMetAsnAspLeuSerGly 522
QY 1638 AACTGTGGTATAGTCAATCAGGATACACACAGTGTGAAGCTGACAATCTGCAGTGGGA 1697
Db 523 AsnCysGlyValThrProThrGlyPheThrProCysThrSerGluAsnValArgCysGly 542
QY 1698 AAATTAATATGTAATATATAGTAAATTTTATTACAAATTTCCAAAGACCATATTATT 1757
Db 543 LysLeuLeuCysThrThrThrAspLysArgGluValIleSerValGluAsnAlaSerValMet 562
QY 1758 TATGCCAACATAAGTGGACATCTCTGCATTCGTGCGAATTTGCCAGTGTATCATGACAG 1817
Db 563 TyrSerAsnIleAsnGlyLysIleCysIleGlyLeuHisTyrGlyTyrGlyAsnGluAsp 582
QY 1818 AGCCAAAAGATGTGAATAAAGATGCAACTCTTGTGGTTTCAAAATGAAGTTTGCAGGAAT 1877
Db 583 GluGlyMetMetThrValLysAspGlyThrValCysGlyGluSerLysIleCysGlnAsn 602
QY 1878 CAAAGATGTGTGATGTTCTTCATCTTGGGTATGATTTGATGTACTACTGACAAATCAATGAT 1937
Db 603 LysGlnCysValAspSerSerPheLeuAsnTyrAspCysAsnProGluLysCysAsnAsn 622
QY 1938 AGAGGTGTATGCAATTAACAAAAGCACTGTCACTGTAGTGTCTCATATTTTACCTCCAGAT 1997
Db 623 GlnGlyValCysAsnAsnLysLysHisCysHisCysAsnProSerTyrLeuProProAsn 642
QY 1998 TGCTCAGTCAATCAGATCTATGCGCTGTGGAGTATTGACAGTGGCAATTTTCCACCT 2057
Db 643 CysGluHisSerAlaProGlyTyrGluGlyGlySerIleAspSerGlyAsnPheProPro 662
QY 2058 GTAGCTATACCA-----GCCAGACTCCCTGAA 2084
Db 663 SerGluProProThrGlyGlyProAlaPheThrAspValGlyThrThrProLeuAlaGlu 682
QY 2085 AGCGCTTACATTGAGAACATTTACCAATTCCAAACCAATGAGATGGCCATTTTCTTATTC 2144
Db 683 SerArgTyrIleGluAsnValTyrArgSerLysProThrArgTyrProPhePheLeuPhe 702
QY 2145 ATTCTCTTCTTATTTTCTGTGCTGATGCTATATGCTGAAGTAAATTTTCCAA 2204
Db 703 IleProPhePheIleIleLeuCysValLeuAlaThrLeuValLysValTyrPheGln 722
QY 2205 AGAAAAAATGGAGAACTGAGGACTATTCAAGCGATGAGCAACCTGAAAGTGAAGTGAA 2264
Db 723 ArgLysLysTyrArgThrGluAspTyrThrSerAspGluGlnLeuGluSerGluSerGlu 742
QY 2265 CCTAAA 2270
Db 743 ProLys 744
```


CC -|- DOMAIN: A tripeptide motif (NOE) within disintegrin-like domain
 CC could be involved in the binding to egg integrin receptor and thus
 CC could mediate sperm/egg binding (By similarity).
 CC -|- PTM: The prodomain and the metalloprotease domain are cleaved
 CC during the epididymal maturation of the spermatozoa (By
 CC similarity).
 CC -|- SIMILARITY: Belongs to peptidase family M12B.
 CC -|- SIMILARITY: Contains 1 disintegrin domain.
 CC -|- SIMILARITY: Contains 1 EGF-like domain.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; X95794; CAA68127.1; ALT_INIT.
 DR HSSP; P18619; LFVL.
 DR MEROPS; M12.950; -.
 DR RGD; 69299; Adam2.
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR008994; Nucleic acid OB.
 DR InterPro; IPR001590; Peptidase M12B.
 DR InterPro; IPR002870; Peptidase M12B_N.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01582; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS50215; ADAM_MEROPS; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF 1; FALSE_NEG.
 DR PROSITE; PS01186; EGF 2; FALSE_NEG.
 DR PROSITE; PS50026; EGF 3; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 18 Potential.
 FT PROPEP 19 180 By similarity.
 FT CHAIN 181 737 ADAM 2.
 FT DOMAIN 19 688 Extracellular (Potential).
 FT TRANSMEM 689 709 Potential.
 FT DOMAIN 710 737 Cytosolic (Potential).
 FT DOMAIN 184 381 Metalloprotease-like.
 FT DOMAIN 389 481 Disintegrin-like.
 FT DOMAIN 482 616 Cys-rich.
 FT DOMAIN 617 650 EGF-like.
 FT DISULFID 293 376 By similarity.
 FT DISULFID 335 360 By similarity.
 FT DISULFID 441 457 Potential.
 FT DISULFID 612 632 By similarity.
 FT DISULFID 626 638 By similarity.
 FT DISULFID 640 649 By similarity.
 FT CARBOHYD 128 128 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 226 226 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 359 359 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 464 464 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 491 491 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 571 571 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 737 AA; 82310 MW; 647E92A9D07CC1D1 CRC64;

Alignment Scores:

Pred. No.: 6, 78-179 Length: 737
 Score: 2479.50 Matches: 442
 Percent Similarity: 75.30% Conservative: 116
 Best Local Similarity: 59.65% Mismatches: 170

Query Match:	51.70%	Indels:	13
DB:	1	Gaps:	6
US-10-054-683-18 (1-2640) x AD02_RAT (1-737)			
QY 72	ATGTGGCTCTTGTCTCTG	-----CTCAGCGGGCTCGCGGGCTG	-----110
DB 1	MetTyrLeuLeuLeuLeuLeuSerGlyLeuSerArgLeuGlyGlyLeuSerGluPro	20	
QY 111	CGGATGGACAGTAATTTTCATAGTTTACCTGCGCAATTTACAGTTCCCGGAGAAATACGG	170	
DB 21	GlnThrGluGlyThrArgGluLeuHisValGlnValThrValProGluLeuSerArg	40	
QY 171	TCAATAATAAAGGAGGAGTCAATCGCAGGCATCTCTACAAATTTGTAATCAAGGAGAA	230	
DB 41	SerIleThrSerGluGlyTyrGluThrGlnValThrTyrSerLeuLeuGlyGlyLeu	60	
QY 231	CCATATCTGTGAATTTAATGCAAAAAAATTTTACCCATAAATTTTAGAGTTTACAGT	290	
DB 61	ThrTyrIleLeuAsnLeuMetGlnLysAlaPheLeuProAsnPheArgValTyrSer	80	
QY 291	TATAGTGGCAGGAGTATTAAGAACCACTTGCACAGATTTTCAGAAATTTCTGCCACTAC	350	
DB 81	TyrAspSerThrGlyIleMetArgProLeuGluGlnLysPheGlnAsnIleCysTyrPhe	100	
QY 351	CAAGGTATATTGAAGTTTATCCAAATCTGTGGTGATGTTAGCACATGTTACTGCACTC	410	
DB 101	GlnGlyTyrIleGluGlyTyrProAsnSerMetValIleValSerThrCysThrGlyLeu	120	
QY 411	AGGGCGTACTACAGTTTCAAAATGTTATGGAATAGAACCCCTGAGAGTTCTTCAGTT	470	
DB 121	ArgGlyValLeuGlnPheGlyAsnValSerTyrGlyIleGluProLeuGluSerSer	140	
QY 471	GGCTTTGACATGTAATTTACCAAGCTAAACATAGAAAGCAGATGTTTCTTATATAAT	530	
DB 141	GlyPheGluHisValIleTyrGlnValGluProLysLysGlyAspThrLeuLeuVal	160	
QY 531	GAGAAGCATATTGAATCAAGAGATCTGCTCTTAAATTAATAAGCGCAGCCACAGCA	590	
DB 161	GluLysAspMetAspLeuArgProGlnTyrLysIleArgSerIleLysProGlnArg	180	
QY 591	GATTTTGAAGTATATAGAAATGCAATGTTATGTTAGTTGAAACAAATGTTATCATG	650	
DB 181	ThrValSerHisTyrLeuGluIleHisIleValValGluLysGlnMetPheGluHisIle	200	
QY 651	GGCTCTGATACACTGTTGCTCAAAAGTTTCCAGTTGATTTGAGTTGAGCAATGCT	710	
DB 201	GlyAlaAspThrAlaValThrGlnLysIlePheGlnLeuIleGlyLeuThrAsnAla	220	
QY 711	ATTTTGTCTTCAATTAATTTACATATTCTGCTCTTCAATTTGAGCTTTGGATAGTAA	770	
DB 221	IlePheAlaProPheAsnLeuThrValIleLeuSerSerLeuGluPheTrpMetAspGlu	240	
QY 771	AATAAATTCGAACCACTGAGAGAGCTAATAGATTATACACATTTTAAAGTGGAA	830	
DB 241	AsnLysIleSerThrThrGlyAspAlaAsnLeuLeuLeuTyrArgPheLeuTyrLys	260	
QY 831	ACATCTTCTCTGTTTCTGCTCTCATGATGTCGCAATTTTCTGTTTACAGAGAAAG	890	
DB 261	GlnSerTyrLeuValLeuArgProHisAspMetAlaPheLeuLeuValTyrArgAspThr	280	
QY 891	TCAATATATGTTGGTCAACCTTTTCAAGGGAAGATGTGATGCAACATATGAGAGGT	950	
DB 281	ThrAspTyrValGlyAlaThrTyrGlnGlyLysMetCysAspLysAsnTyrAlaGly	300	
QY 951	GTTGTTCTGACCCCAAGACCATAGTCTGATCATCTTTCAGTTTATTTAGTCAATTA	1010	
DB 301	ValAlaLeuHisProLysAlaValThrLeuGluSerLeuAlaIleLeuValGlnLeu	320	
QY 1011	TTGAGCTTATGTTGGGATCTTATGATGACATTAACAAATGCCAGTCTCTCAGGAGCT	1070	
DB 321	LeuSerLeuSerMetGlyValAlaTyrAspAspValAsnThrCysGlnCysGlyValPro	340	

QY 1071 GTCTGCAATTATGATTCAGAGCAATTCATTTCAGTGGTGTGAAGATCTTTAGTAAGTC 1130
Db ::
QY 341 IleCysValMetAsnProGluAlaLeuHisSerGlyValArgSerPheSerAsnCys 360
QY 1131 AGCTTCGAAGACTTTGACACATTTTATTTCAAAGCAGAAAGTCCCACTGCTCTTCACAAATCAG 1190
Db ::
QY 361 SerMetGluAspPheSerLysPheIleValSerGlnSerSerHisCysLeuGlnAsnGln 380
QY 1191 CTTGCTTAGATCTTTTTCAAACAGCAAGCAGTGTGTGTAAATGCAAGCTGGAAGCA 1250
Db ::
QY 381 ProHisLeuGlnProSerTyrLys---MetAlaValCysGlyAsnGlyGluLeuGluGlu 399
QY 1251 GCGAGAGTGTGACTGCGGACTGAACAGGATGTGCCCTTATTGAGAAACATGCTGT 1310
Db ::
QY 400 GlyGluValCysAspCysGly---GlnGluGlyCysAspAspLysProProCysCys 418
QY 1311 GATATTCACATGTAGATTAAAGCGGTTCAAACCTGTGCTGAAGCACCATGCTGGAA 1370
Db ::
QY 419 AsnProThrThrCysGlnLeuSerGluGlySerThrCysSerThrGlySerCysAsp 438
QY 1371 ---AAGTGTCTATTGTCAAAGAAAGATGTGTAGGCTTCTCTTTGAAGATGCGAC 1427
Db ::
QY 439 AlaSerCysAsnLeuLysAlaLysGlyGluLeuCysArgProAlaAsnGlnCysAsp 458
QY 1428 CTCCTGAATATTCGATGCATCTGCATCATGCCAGAAACCACTATGTTCACT 1487
Db ::
QY 459 ValThrGluTyrCysAsnGlyThrSerGluValCysGluGluAspPhePheValGlnAsp 478
QY 1488 GGGCATCCGTGTGAGTCAATCAATGATCTGTATAGATGGAGTTTCTATGAGTGGGAT 1547
Db ::
QY 479 GlyHisProCysAlaGluGlnLysTrpIleCysIleAsnGlyThrCysGlnSerGlyAla 498
QY 1548 AACAATGTACAGACACATTTGGCAAGAAGTAGTGAGTTTGGCCCTTCAGAAATGTTATCT 1607
Db ::
QY 499 GlnGlnCysArgAspLeuPheGlyThrAspAlaAspTyrGlyThrLysGluCysTyrSer 518
QY 1608 CACCTTAATTCAGAGCTGATGATCTGGAACCTGCTGATAGTATGATTCAGGATACACA 1667
Db ::
QY 519 GluLeuAsnSerLysSerAspIleSerGlySerCysGlyIleThrProThrGlyTyrLys 538
QY 1668 CAGTGTGAAGTCAATCTGAGTGGGAAATTAATATGTAATATGATGAGTAAATTT 1727
Db ::
QY 539 AspCysAlaProAsnAspArgMetCysGlyLysLeuIleCysIleTyrGlnSerGluAsp 558
QY 1728 TTATTACAAATCCAGAGCCACTATTATTATTCGCCAACATAAGTGGACATCTCTGCATT 1787
Db ::
QY 559 IleLeuLysMetArgSerAlaIleValIleTyrAlaAsnIleSerGlyGlnIleCysIle 578
QY 1788 GCTGTGGAATTCGAGTATCATCGACAGCAGCAAGATGGGATAAAGATGGAAT 1847
Db ::
QY 579 SerLeuGluTyrProProGlyHisLysGluSerLysMetCysValArgAspGlyThr 598
QY 1848 TCTTGTGGTTCAATAAGTTTGCAGGAATCAAGATGTGTGAGTTCTTCTATCTGGGT 1907
Db ::
QY 599 ValCysGlySerGlyLysValCysLeuAsnGlnGluCysValGluAspThrPheLeuAsn 618
QY 1908 TATGATTGTACTACTGCAAAATGCAATGATAGAGGTGTATGCAATACAAAGACACTGT 1967
Db ::
QY 619 TyrAspCysThrProGluLysCysAsnHisGlyValCysAsnAsnLysLysHisCys 638
QY 1968 CACTGATGCTTCATATTACTTCAGATGCTGATGCTCACTCAATCAGATCTATGCTCGGT 2027
Db ::
QY 639 HisCysGluProThrTyrLeuProProAspCysLysAsnThrGluAspThrTrpProGly 658
QY 2028 GCGAGTATTCAGAGTGGCAATTTTCCACCTGTAGCTATACCCAGCAGACTCCCTGAAAG 2087
Db ::
QY 659 GlySerValAspSerGlyAsnGlnArgAla-----GluSerIleProAlaArg 675
QY 2088 CGGTACATTGAGCAATTTTACCATTTCCAAAACCAATGAGTGGCATTTTCTTATTCTATT 2147
Db ::
QY 676 SerTyrValAlaSerAlaTyrArgSerLysSerAlaArgTrpProPhePheLeuIle 695
QY 2148 CCTTCTCTTATTTTCTGTGACTGATGCTATATGTTGTAAGTGAAGTAATTTCCAAAG 2207

Db 696 ProPheTyrValValIleLeuValLeuIleGlyMetLeuValLysValTyrSerGlnArg 715
QY 2208 AAAAAATGGAGACTGAGTCACTATTCAAGGAGTGAAGCACTGAAAGTGAAGTGAACCT 2267
Db ::
QY 716 LysLysTrpArgMetAspPheSerSerGluGluGlnPheGluSerGluSerGluSer 735
Db 2268 AAA 2270
Db 736 Lys 736
RESULT 9
AD02_MOUSE STANDARD; PRT; 735 AA.
AC Q60718; Q60814; Q9D4G3; Q9QWJ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30) (PH30) (PH30-beta).
GN Names=Adam2; Synonyms=Ftnb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MSDLINE=9601260; PubMed=7593287;
RA Evans J.P., Schultz R.M., Kopf G.S.;
RT "Mouse sperm-egg plasma membrane interactions: analysis of roles of
RT egg integrins and the mouse sperm homologue of PH-30 (fertilin)
RL beta.";
RL J. Cell Sci. 108:3267-3278(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Gupta S.K., Alves K., Palladino L.O., Mark G.B., Hollis G.F.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=2234683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla S., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hiroxane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE OF 17-735 FROM N.A.

161	GlulysAspIleAspLeuArgAspSerGlnTyrIlysIleArgSerIleLysProGlnArg	180
591	GATTTTGCAGATATAGAAATGCATGTATATAGTTGAAAAACAATGTATATATCATATG	650
181	IleValSerHisTyrLeuGluIleHisIleValValGluLysGlnMetPheGluHisIle	200
651	GGGTCTGATCAACTGTTGTGCGCTCAAAAAGTTTTTCCAGTTGATTGATTGACGAATGCT	710
201	GlyAlaAspThrAlaIleValThrGlnLysIlePheGlnLeuIleGlyLeuAlaAsnAla	220
711	ATTTTTCGTTTCATTATAATTACAAATTTCTGTCCTTCATTGGAGCTTTCGATAGTAGAA	770
221	IlePheAlaProPheAsnLeuThrValIleLeuSerSerLeuGluPheTrpMetAspGlu	240
771	AATAAAATTCGAACCACTGGAGAGCTAAATGAGTTATTACACACATTTTTTAAGATGAAA	830
241	AsnLysIleLeuThrThrGlyAspAlaAsnLysLeuLeuTyrArgPheLeuLysTrpLys	260
831	ACATCTTATCTGTTTTTACGTCTCATGATGTGGCATTTTTTACTTGTGTTTACAGAAAAG	890
261	GlnSerTyrLeuValLeuArgProHisAspMetAlaPheLeuLeuValTyrArgAsnThr	280
891	TCAAAATTTGTTGTGTCAACTTTTCAAGGGAAGATGTGTATGCACAACTATGCAGGAGGT	950
281	ThrAspTyrValGlyAlaThrTyrGlnGlyLysMetCysAspLysAsnTyrAlaGlyGly	300
951	GTTCTTCTGCACCCGACAAACATAAGTCTCGAATCACTTCAGTATTATTTAGTCTCAATTA	1010
301	ValAlaLeuHisProLysAlaValThrLeuGluSerLeuAlaIleIleLeuValGlnLeu	320
1011	TTGAGCCTTAGTATGGGATCATTTATGATGACATTAATCAAAATGCCAGTCTCAGGAGCT	1070
321	LeuSerLeuSerMetGlyLeuAlaTyrAspAspValAsnLysCysGlnCysGlyValPro	340
1071	GTCTGCATTATGAATCCAGAGCAATTCATTTACGTGTGTGAAGATCTTTAGTAACTGC	1130
341	ValCysValMetAsnProGluAlaProHisSerSerGlyValArgAlaPheSerAsnCys	360
1131	AGCTTCCGAAGACTTTGCACATTTTATTTCAAAGCAGAAAGTCCCACTGCTCTTCACAATCAG	1190
361	SerMetGluAspPheSerLysPheIleThrSerGlnSerSerHisCysLeuGlnAsnGln	380
1191	CCTCGCTTAGATCCTTTTTCAAACAGCAAGCAGTGTGTGGTAAATCAAAAGCTGGAAGCA	1250
381	ProArgLeuGlnProSerTyrLys--MetAlaValCysGlyAsnGlyGluValGluGlu	399
1251	GGAGAGAGTGTGACTGTGGCATGCAACAGATTGTCCTTATTGAGAGAAAATGCTGT	1310
400	AspGluIleCysAspCysGly--LysLysGlyCysAlaGluMetProProCysCys	418
1311	GATATTGCCACATCTAGATTTAAAGCCGGTTTCAAACGTGCTGAAGACCACTGTCGGAA	1370
419	AsnProAspThrCysLysLeuSerAspGlySerGluCysSerSerGlyIleCysCysAsn	438
1371	AACTGCTTATTATGTCAAAAGAAAGAAATGTGTAGGCTCTTCCTTTGAAGAATGCGACCTC	1430
439	SerCysLysLeuLysArgLysGlyGluValCysArgLeuAlaGlnAspGluCysAspVal	458
1431	CCTGAATATTGCAATGGATCATCTGCATCATGCCCAAGAAACCACTATGTTTCAGACTGGG	1490
459	ThrGluTyrCysAsnGlyThrSerGluValCys---GluAspPhePheValGlnAsnGly	477
1491	CATCCGNTGGACTGAATCAATGATCTGTATAGATGGAGTTTGTATAGTGGGGATAAA	1550
478	HisProCysAspAsnArgLysIleTrpIleCysIleAsnGlyThrCysGlnSerGlyGluGln	497
1551	CAATGTACACACATTTGGCAAAAGTAGATTTGGCCCTTCAGAAATGTTATCTTCAC	1610
498	GlnCysGlnAspLeuPheGlyIleAspAlaGlyPheGlySerSerGluCysPheTrpGlu	517
1611	CTTAATTCAAAGACTGATGATATCTGGAAACTGTGGTATAGATGATTCAGGATACACAG	1670
518	LeuAsnSerLysSerAspIleSerGlySerCysGlyIleSerAlaGlyLysLysGlu	537

Qy	1671	TGTGAGCTGACAACTCGACAGTGGCGGAAANATTAATATGTAATAATGTAGGTAAATTTT	1730
Db	538	CysProAsnAspArgMetCysGlyLysIleleCysLysTyGlnSerGluAsnIle	557
Qy	1731	TTACAAATTTCCAAGAGGACCTATTATTATTATGCGCAACAAAGTAGTGACATCTCTGCATTGCT	1790
Db	558	LeuLysLeuArgSerAlaThrValIleTyAlaAsnIleSerGlyHLeValCysValSer	577
Qy	1791	GTGGAATTTGCCATGTCATGCAGACAGCCAAAGATGTGGATAAAAGATGGAACCTTCT	1850
Db	578	LeuGluTyProGlnGlyHisAsnGluSerGlnLysMetTrpValArgAspGlyThrVal	597
Qy	1851	TGTGGTTCAATAAGGTTTCGACGAATCAAGATGTGTGAGTCTTCATACTTGGGTTAT	1910
Db	598	CysGlySerAsnLysValCysGlnAsnGlnLysCysValAlaAspThrPheLeuGlyTy	617
Qy	1911	GATTGTACTACTGACAAATGCAATGATAGAGGTGTATGCAATTAACAAAAAGCACTGTCCAC	1970
Db	618	AspCysAsnLeuGluLysCysAsnHisGlyValCysAsnAsnLysLysAsnCysHis	637
Qy	1971	TGTAAGTGCTTCATATTTACTTCAGATTGCTCTGACTTCAATCAGACTATATGGCTGTGGGG	2030
Db	638	CysAspProThrTyLeuProCaspCysLysArgMetLysAspSerTyProGlyGly	657
Qy	2031	AGTATTCACAGTGGCAATTTTCCACCTGTAGCTATACAGCCAGACTCCCTGAAAGCGC	2090
Db	658	SerIleAspSerGlyAsn---LysGluArgAlaGluPro-----IleProValArgPro	674
Qy	2091	TACATTGAGAACATTTACCATTCCAAACCAATGAGATGGCGCATTTTCTTATTCAATCTCT	2150
Db	675	TyrIleAlaSerAlaTyArgSerLysSerProArgTrpProPheLeuLeuIlePro	694
Qy	2151	TTCTTTATATTTTCTGTGACTGATTGCTATATATGTGTAAAGTTAATTTCCAAAGGAA	2210
Db	695	PheTyValValIleLeuValLeuIleGlyMetLeuValLysValTySerGlnArgMet	714
Qy	2211	AAATGGAGAACTGAGGACTTCAAGCGATGACGACCACTCAAAAGTGAGAGTGAACTAAA	2270
Db	715	LysTrpArgMetAspAspPheSerSerGluGluGlnPheGluSerGluSerLys	734
RESULT 10			
ID	AD02_CAVPO	STANDARD;	PRT; 735 AA.
AC	Q60411,		
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	05-JUN-2004	(Rel. 44, Last annotation update)	
DE	ADAM 2 precursor	(A disintegrin and metalloproteinase domain 2)	
DE	(Fertilin beta subunit)	(PH-30) (PH30).	
GN	Name=ADAM2; Synonyms=FTNB;		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.		
OX	NCBI_TaxID=10141;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUR=Testis;		
RX	MEDLINE=94068486; PubMed=8248170;		
RA	Wolfsberg T.G., Bazan J.F., Blobel C.P., Myles D.G., Primakoff P.,		
RA	White J.M.;		
RT	"The precursor region of a protein active in sperm-egg fusion contains		
RT	a metalloprotease and a disintegrin domain: structural, functional,		
RT	and evolutionary implications.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 90:10783-10787(1993).		
RN	[2]		
RP	SEQUENCE OF 383-735 FROM N.A.		
RC	TISSUR=Testis;		
RX	MEDLINE=92204234; PubMed=1552944;		
RA	Global C.P., Wolfsberg T.G., Turk C.W., Myles D.G., Primakoff P.,		
RA	White J.M.;		
RT	"A potential fusion peptide and an integrin ligand domain in a protein		
RT	active in sperm-egg fusion.";		

DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS02015; ADAM MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS02014; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 KW EGF-like domain; Glycoprotein; Signal; Spermatogenesis; Transmembrane.
 FT SIGNAL 1 16
 FT PROPEP 17 183
 FT CHAIN 184 746
 FT DOMAIN 177 687
 FT TRANSMEM 688 708
 FT DOMAIN 709 746
 FT DOMAIN 184 389
 FT DOMAIN 390 479
 FT DOMAIN 480 619
 FT DOMAIN 620 654
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 FT DISULFID 458 483
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 FT CARBOHYD 294 294
 FT CARBOHYD 359 359
 FT CARBOHYD 465 465
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 SQ SEQUENCE 746 AA; 84448 MW; 1D8C7E907150ZE30 CRC64;
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 Score: 1586.50 Matches: 310
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 Query Match: 33.08% Indels: 35
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 QY 75 TGGTCTGTTCTGCTCAGCGGCTGGCGGCTGGGATGGAGTAAATTTTCATAGT 134
 DB 3 PheLeuLeuAlaLeuLeuThrGluLeuGlyArgLeuGlnAlaHisValGlySerGluGly 22
 QY 135 TTACCTGTGCAATACAGTTCCGGAGAAATACGGTCAATAATAAGGAGGAATGAA 194
 DB 23 IlePheLeuHisValThrValProArgLysIleLeuSerAsnAspSerGluValSerGlu 42
 QY 195 TCGCAGCATCCTCAAAATTTGTAATGAAGGAAACCATATCTACTGTGAATTTAATGCAA 254
 DB 43 ArgLysMetIleTyrlleIleThrIleAspGlyGlnProTyThrLeuHisLeuArgLys 62
 QY 255 AAAAATTTTACCCCAATTTTACAGTTTACAGTTTACAGTTTACAGTTTACAGTTTACAA 314
 DB 63 GlnSerPheLeuProGlnAsnPheLeuValTyThrTyThrAsnGluAlaGlySerLeuHis 82
 QY 315 CCACTTGACCAAGATTTTCAGAAATTTCTGCACATACCAAGGATATTTGAAGGTTATCCA 374
 DB 83 SerGlnSerProTyThrPheMetMetHisCysHisTyThrGlnGlyTyAlaAlaGluPhePro 102
 QY 375 AAATCTGTGGTAGGTAGACATGTAAGTCTGAGTCTGAGGCGGCTACTGATGTTGAAAT 434
 DB 103 AsnSerPheValThrLeuSerIleCysSerGlyLeuArgGlyPheLeuGlnPheGluAsn 122
 QY 435 GTTAGTTATGAAATAGAACCCCTGAGTCTTACGTTTGGCTTTGACATGTAATTTACCA 494
 DB 123 ValSerTyrrGlyIleGluProLeuGluSerSerAlaArgPhePheGluHisIleIleTyrrGln 142

QY 495 GTAACACATAAGAAAGCAGATGTTTCTCTATAT-----AATGAGAAGGATATGAATCA 548
 DB 143 MetLysAsnAsnAspProAsnValSerIleLeuAlaGluAsnTyrrSerHisIleTyrrGln 162
 QY 549 AGAGATCTGCTCTTAAATATCAAAAGCGCAGAGCCACAGCAAGATTTTGGCAAG----- 602
 DB 163 LysAspGlnSerTyrrLysValProLeuAsnSerGlnLysLysAsnLeuSerLysLeuLeu 182
 QY 603 -----TATATAGAAATGTCATGTTATAGTTGAAACAAATTTGATATATCATATGGGCTCT 656
 DB 183 ProGlnTyrrLeuGluIleTyrrIleValGluLysAlaLeuTyrrAspTyrrMetGlySer 202
 QY 657 GATCAACACTGTCGCTCAAAAGTTTCCAGTTGATTTGATTTGATTTGATTTGATTTT 716
 DB 203 GluMetMetAlaValThrGlnLysIleValGlnValIleGlyLeuValAsnThrMetPhe 222
 QY 717 GTTTCATTTAATATTAATATTATTTCTCTCTTCAATTGGAGCTTTGGATAGATGAAATAAA 776
 DB 223 ThrGlnPheArgLeuThrValThrLeuSerSerLeuGluLeuTrpSerAsnGluAsnGln 242
 QY 777 ATTGCACCACTGGAGAGCTAATAGTTATTACACACATTTTAAGATGGAACATCT 836
 DB 243 IleSerThrSerGlyAspAlaAspAspIleLeuGlnArgPheLeuAlaTrpLysArgAsp 262
 QY 837 TATCTTGTCTTCT 896
 DB 263 TyrrLeuIleLeuArgProHisAspIleAlaTyrrLeuLeuValTyrrArgLysHisProLys 282
 QY 897 TATGTGGTCAACCTTTCAAGGAGATGTGTGATGCAAACTATGCAAGGAGTTGTT 956
 DB 283 TyrrValGlyAlaThrPheProGlyTyrrIleCysAsnGluSerTyrrAspAlaGlyIleAla 302
 QY 957 CTGCACCCAGAACCACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1016
 DB 303 MetTyrrProAspAlaIleAspLeuGluGlyPheSerValIleIleAlaGlnLeuLeuGly 322
 QY 1017 CTTAGTATGGGATCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076
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 QY 1077 ATTATGAATCCAGAACATTTCAATTTCAAGTGTGTGATGATGATGATGATGATGATGATGAT 1136
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 DB 383 LeuGlnProLeuHisGlnAsnGlnProValCysGlyAsnGlyIleLeuGluSerAsnGlu 402
 QY 1257 GAGTGTGCTGTGGGACTGAACAGGATTTGCCCTTATTTGGAGAAACATGCTGTGATATT 1316
 DB 403 GluCysAspCysGlyAsnLysLysGluCysGlnPhe-----LysLysCysAspTyrr 420
 QY 1317 GCCACATGTAGATTTAAAGCCGTTCAAACTGCTGCTGAAGCACCCTCTGCTGCTGCTGCTGCT 1373
 DB 421 AsnThrCysLysLeuLysGlySerValLysCysGlySerGlyProCysTyrrSerLys 440
 QY 1374 TGCTTATTTATGTCAAAGAAAGAAATGCTGTAGGCTTCTCTTTGAA-----GAATGCGACCTC 1430
 DB 441 CysGluLeuSerIleValGlyThrProCysArgLysSerValAspProGluCysAspPhe 460
 QY 1431 CTGGAATATTGCAATGATCATCTGCATCATGCCGAAACCACTATGTTTCAGATCGG 1490
 DB 461 ThrGluTyrrCysAsnGlyThrSerSerAspCysValProAspThrTyrrAlaLeuAsnGly 480
 QY 1491 CATCCGTGTGCTGAATCAATGATCTGTATAGATGAGTCTTGTATGATGCTGGGATAAA 1550
 DB 481 HisLeuCysLysLeuGlyThrAlaTyrrCysTyrrAsnGlyGlnCysGlnThrThrAspAsn 500

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QY 1551 CAAATGTACACACATTTGGCAAGAGTAGTGGCTTGGCCCTTCAGAAATGTTATTCAC 1610
D 1551 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 501 GlnCysAlaLysLePheGlyLysGlyAlaGlnGlyAlaProPheAlaCysPheLysGlu 520
QY 1611 CTTAAATCAAGACTGATCTATCGAACTGTGGTAAAGTGAATTCAGGATACACACAG 1670
D 1611 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 521 ValAsnSerLeuHisGluThrSerGluAsnCysGlyPheLysAsnSerGlnProLeuPro 540
QY 1671 TGTGAAGCTGCAATCTGCAGTGGGAAATTAATATGTAATATGATGAGTAATTTTA 1730
D 1671 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 CysGluArgLysAspValLeuCysGlyLysLeuAlaCysValGlnProHisLysAsnAla 560
QY 1731 TTACAATTCAGAGCCATATATTTATGCCAACAATAGTGGACATCTCTCATGCT 1790
D 1731 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 561 TyrLysSerAspLeuGlnThrValThrValThrValThrValThrValThrValThr 580
QY 1791 GTG-----GAATTTGCCAGTGATCATGCACAGACAGCCAAAGATGTGATAAAA 1838
D 1791 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 581 IleAlaThrGlySerSerMetArgSerAspGlyThrAspAsn-----AlaThrValAla 598
QY 1839 GATGGAACCTTCTGTGTTCAAAATAGGTTTGCAGGAAATCAAGATGTGTGAGTTCTTCA 1898
D 1839 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 599 AspGlyThrMetCysGlyProGluMetTyrCysValAsnLysThrCysArgLysValHis 618
QY 1899 TACTTGGTTATGTTGT-----ACTACTGACAATGCAATGATGAGTGTATGCAATAAC 1955
D 1899 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 619 LeuThrGlyTyrAsnCysAsnThrThrThrLysCysLysGlyLysGlyLysCysAsnAsn 638
QY 1956 AAAAAGCAGTCACTAGTCTGCTTCATATTTACCTCCAGTCTCAGTTCATCAGAT 2015
D 1956 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 639 PheGlyAsnCysGlnCysPheProGlyHisLysProAspCysLysPheGlnPheGly 658
QY 2016 CTATGGCTGTGGAGTATTGACAGTGGCAATTTTCCACCTGTAGTATACCAGGCAGA 2075
D 2016 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 659 Ser---ProGlyGlySerIleAspAspGlyAsnPhe-----Gln 670
QY 2076 CTCCTGGAAGGGCTACATGAGACATTTACCATTCCAAACCATGAGATGG----- 2129
D 2076 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 671 LysSerAspGluPheThrGluLysGlyTyrAsnAlaHisTrpAsnAsnTrpPheIle 690
QY 2130 ---CCATTTTCTTATTCATCTCTCTTCTTATTTATTTCTGCTGCTGCTGCTGCTGCT 2186
D 2130 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 691 LeuSerPheThrIleValLeuProPheIleIleIleIleIleIleIleIleIleIleIle 707
QY 2187 GTGAAAGTTAATTTCCAAAGGAAAAATGAGGA 2219
D 2187 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 708 -----PheLysArgAsnGluIleArg 714

RESULT 12
AD18_HUMAN STANDARD; PRT; 739 AA.
AC Q9Y307;
CT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE ADAM 18 precursor (A disintegrin and metalloproteinase domain 18)
DE (Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-
DE rich protein III) (tMDC III).
GN Name=ADAM18; Synonyms=tMDC3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hall L., Frayne J., Dimsey E.A.;
RT "Nucleotide sequence of the human tMDC III sperm surface protein
RT transcript."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sperm surface membrane protein that may be involved in
CC spermatogenesis and fertilization. This is a non catalytic
CC metalloproteinase-like protein (By similarity).

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CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed specifically in testis.
CC DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding (By similarity).
CC -!- PTM: The prodomain and the metalloproteinase-like domain are cleaved
CC during the epididymal maturation of the spermatozoa (By
CC similarity).
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ133004; CAB40812.1; -.
CC HSPB; P83469; IMPZ.
CC DR MEROPS; M12.957; -.
CC DR Genew; HGNC:196; ADAM18.
CC DR GO; GO:0005624; C:membrane fraction; TAS.
CC DR GO; GO:0008237; F:metalloproteinase activity; TAS.
CC DR GO; GO:0007283; P:spermatogenesis; TAS.
CC DR InterPro; IPR006586; ADAM cysteine.
CC DR InterPro; IPR001762; Disintegrin.
CC DR InterPro; IPR006209; EGF-like.
CC DR InterPro; IPR001590; Peptidase_M12B.
CC DR InterPro; IPR002870; Peptidase_M12B_N.
CC DR Pfam; PF00200; Disintegrin; 1.
CC DR Pfam; PF01562; Pep M12B propep; 1.
CC DR Pfam; PF01421; Reprolysin; 1.
CC DR ProDom; PD000664; Disintegrin; 1.
CC DR SMART; SM00608; ACR; 1.
CC DR SMART; SM00050; DISIN; 1.
CC DR PROSITE; PS00215; ADAM MBPRO; 1.
CC DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
CC DR PROSITE; PS00214; DISINTEGRIN_2; 1.
CC DR PROSITE; PS00022; EGF_1; FALSE_NEG.
CC DR PROSITE; PS01186; EGF_2; FALSE_NEG.
CC KW EGF-like domain; Glycoprotein; Signal; Spermatogenesis; Transmembrane.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 184 Potential.
FT CHAIN 185 739 ADAM 18.
FT DOMAIN 177 687 Extracellular (Potential).
FT TRANSMEM 688 708 Potential.
FT DOMAIN 709 739 Cytoplasmic (Potential).
FT DOMAIN 177 389 Metalloproteinase-like.
FT DOMAIN 390 479 Disintegrin-like.
FT DOMAIN 480 622 Cys-rich.
FT DOMAIN 620 654 EGF-like.
FT DISULFID 293 376 By similarity.
FT DISULFID 335 360 By similarity.
FT DISULFID 458 483 Potential.
FT DISULFID 624 636 By similarity.
FT DISULFID 630 642 By similarity.
FT DISULFID 644 653 By similarity.
FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 149 149 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 156 156 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 294 294 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 359 359 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 465 465 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 561 561 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 611 611 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 625 625 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 739 AA; 82856 MW; 2D8BE9A975072CDD CRC64;

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Alignment Scores:				
Pred. No.:	5.06e-111	Length:	739	
Score:	1582.50	Matches:	314	
Percent Similarity:	58.93%	Conservative:	128	
Best Local Similarity:	41.87%	Mismatches:	275	
Query Match:	33.00%	Indels:	33	
DB:	1	Gaps:	13	
US-10-054-683-18 (1-2640) x AD18_HUMAN (1-739)				
QY	78	GTCTCTGTTCTGCTCAGCGGCTCGCGGGCTGGGATGACAGTAAATTTTGATAGTTA	137	
DB	4	LeuLeuAlaLeuLeuThrGluLeuGlyArgLeuGlnAlaHisGluGlySerGluGlyIle	23	
QY	138	CTGTGCAAAATTACAGTTCGGAGAAATACGGTCAATAATAAAGGAAGGAATGCAATCG	197	
DB	24	PheLeuHisValThrValProArgLysIleLysSerAsnAspSerGluValSerGluArg	43	
QY	198	CAGGCATCTCAAAATTTGTAATTGAAGGAAACCATATCTGTGCAATTTAATGCAAAA	257	
DB	44	LysMetIleTyrIleIleThrIleAspGlyGlnProTyrThrLeuHisLeuGlyLysGln	63	
QY	258	AACCTTTTACCCATAATTTTAGAGTTTACAGTTATAGTGGCACAGGAATTTATGAACA	317	
DB	64	SerPheLeuProGlnAsnPheLeuValTyrThrTyrAsnGluThrGlySerLeuHisSer	83	
QY	318	CTTGACCAAGATTTTCAGAAATTTCTGCCACTACCAAGGTATATTGAAGTTATCCAAA	377	
DB	84	ValSerProTyrPheMetMetHisCysHisTyrGlnGlyTyrAlaAlaGluPheProAsn	103	
QY	378	TCTGTGTGATGTTAGCACATGACTGACTCAGGGCGTACTACAGTTTGAATGCTT	437	
DB	104	SerPheValThrLeuSerIleCysSerGlyLeuArgGlyPheLeuGlnPheGluAsnIle	123	
QY	438	AGTTATGGAATAGAACCCCTGGAGTCTTCAGTGGCTTTGAACATGTAATTTACCAAGTA	497	
DB	124	SerTyrGlyIleGluProValGluSerSerAlaArgPheGluHisIleIleTyrGlnMet	143	
QY	498	AAACATAAGAAAGACAGATGTTTCCTTA-----TATATGAGAGGATATTGAATCAAGA	551	
DB	144	LysAsnAsnAspProAsnValSerIleLeuAlaValAsnTyrSerHisIleTyrGlnLys	163	
QY	552	GATCTGCTCTTAAATTACAAAGCGCAGAGCCAGCAAGATTTTGCAAG-----602		
DB	164	AspGlnProTyrLysValProLeuAsnSerGlnIleLysAsnLeuSerLysLeuLeuPro	183	
QY	603	---TATATAGAAATGCATGTTATAGTTGAAACAAATTTGTAATATATATGCGGTCTGAT	659	
DB	184	GlnTyrLeuGluIleTyrIleIleValGluLysAlaLeuTyrAspTyrMetGlySerGlu	203	
QY	660	ACAATGTTGCTGCAAAAGTTTTCAGTTGATGAGTTCAGCAATGCTATTTTGT	719	
DB	204	MetMetAlaValThrGlnLysIleValGlnValIleGlyLeuValAsnThrMetPheThr	223	
QY	720	TCATTTAATATTACAAATTTCTGCTTCATGAGCTTTGCAATGATGAAATAAAAT	779	
DB	224	GlnPheLysLeuThrValIleLeuSerSerLeuGluLeuTyrSerAsnGluAsnGlnIle	243	
QY	780	GCAACCACTGGAGAGCTAATGATTATTACACATTTTAAAGATGGAACATCTTAT	839	
DB	244	SerThrSerGlyAspAlaAspAspIleLeuGlnArgPheLeuAlaTyrLysArgAspTyr	263	
QY	840	CTTGTGTTTACCTCTCATGATGGCATTTTACTTGTGTACAGAGAAAGTCAAAAT	899	
DB	264	LeuIleLeuArgProHisAspIleAlaTyrLeuLeuValTyrArgLysHisProLysTyr	283	
QY	900	GTTGGTCAACCTTTCAAGGGAAGATGTGTGATGCAAACTATGCAAGAGGTGTTCTG	959	
DB	284	ValGlyAlaThrPheProGlyThrValCysAsnLysSerTyrAspAlaGlyIleAlaMet	303	
QY	960	CACCCAGAACCATTAAGTCTGGAATCACTTCAGTATTATTTAGCTCAATTTATGAGCCTT	1019	

QY 420 CTACAGTTTCAAAATGTTAGTTATGGAATAGAACCCCTGGAGTCTTTCAGTTGGCTTTGAA 479
Db 121 LeuGlnPheGluAenValSerTyrGlyLeuProLeuGluSerAlaValGluPheGln 140
QY 480 CATGTATTTTACCAAGTAACATAAGAAAGCAGATGTTCTTATATATATGAGAAGGAT 539
Db 141 HisValLeuTyrLysLeuLysAenGluAspAsnAspIleAlaIlePheIleAspArgSer 160
QY 540 ATTGAATCAAGA-----GATCTGCTCTTTAAATTACAAGCGCAGACCCACAGCAA 590
Db 161 LeuLysGluGlnProMetAspAspAsnIlePheIleSerGluLysSerGluProAlaVal 180
QY 591 GAT-----TTTGCAAGTATATAGAAATGCATGTTATAGTTGAAAAACAATTGTATAAT 644
Db 181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspLysThrLeuTyrAsp 200
QY 645 CATATGGGGCTGATACAACTGTTGTCGCTCAAAAAGTTTCCAGTTGATGGATTGACG 704
Db 201 TyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluIleValGlyLeuAla 220
QY 705 AATGCTATTTTGTTCATTTAATATACAAATTATCTGCTTCATTTGGAGCTTTGGATA 764
Db 221 AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGluLeuTrpSer 240
QY 765 GATGAAATAAATTTGCAACCACTGGAGAACTAATGAGTTATTACACACATTTTAAAGA 824
Db 241 AspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuLysPheLeuGlu 260
QY 825 TGGAAAAACATCTTATCTGTTTACGTCCTCATGATGGCAATTTTACTTTGTTTACAGA 884
Db 261 TrpLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaTyrLeuLeuIleTyrMet 280
QY 885 GAAAGCTCAATATGTTGTCGCAACCTTTCAGGGAGAGTGTGTGATGCAAACTATGCA 944
Db 281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
QY 945 GGAGCTGTGTTCTGCAACCCCAACCACTAGTCTGGAATCACATTCAGTTATTTAGCT 1004
Db 301 AlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
QY 1005 CAATATTGAGCCTTAGTATGGGATCACTTATGATGACATTAAACAATGCCAGTGTCTCA 1064
Db 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCysGlnCysSer 340
QY 1065 GGACCTGCTCATTAATGAAATCCAGAACCAATTCATTTACGTGTGTGAGATCTTTAGT 1124
Db 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
QY 1125 AACTGCAGCTTCGAAGACTTTGCACATTTTATTTTCAAGACGAAAGTCCCAAGTCTTTCAC 1184
Db 361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
QY 1185 AATCAGCTCCCTAGATCCTTTTTCACAGACGACGATGTTGTTATGCAAAAGCTG 1244
Db 381 AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
QY 1245 GAAGCAGGAGGAGGTGACTGTGGGACTCAACAGGATTCGCCCTTATTGGAGAACA 1304
Db 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
QY 1305 TGCTGTGATATTGCCACATGTAGATTTTAAAGCCGGTTCAAATCTGCTGCAAGGACCAATGC 1364
Db 418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
QY 1365 TGGCAAACTGCTCTATTATGTCAAAAGAAAGATGTAGCCCT---TCCTTTGAAGAA 1421
Db 438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
QY 1422 TGGCAGCTCCCTGATATTTGCAATGGATCATCTGCATCATGCCAGAAACCACTATGTT 1481
Db 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477

QY 1482 CAGACTGGGCATCCCTGTGGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATGAGT 1541
Db 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGlyAspCysHisAsp 497
QY 1542 GGGGATAACAATGTACACACACATTTGCGAAGAGTAGACTTTTGGCCCTTCAGAAATCT 1601
Db 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
QY 1602 TATTCCTCACTTAATCAAGACTGATGTATCTGGAACCTGTGGTATATAGT---GATTCA 1658
Db 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspAsnAsn 537
QY 1659 GGATACACACATGTGAAGCTGACATCTGCAGTGGGAAATTAATATGTAATATGTA 1718
Db 538 LysTyrValPheCysGlyTyrArgAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
QY 1719 GGTAAATTTTATTACAAATCCAGAGCCACTATTATTATGTCACCAACATAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
QY 1779 CTCTGCAATTCCTGTGGAATTTGCCAGTATCATGCAGACAGCCAAAGATGTGGATAAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
QY 1839 GATGAACTCTTGTGTTCAATAAGTTTCGAGGAATCAAGATGCTGTGAGTTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgLysValGluSerArg 617
QY 1899 TACTTG-----GGTTATGATGTTACTACTACAAATGCAATGATAGAGTGTATGC 1949
Db 618 IleIleGlyAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
QY 1950 AATAACAAAAAGCACTCTCACTGTAGTGTCTCATATTTACCTCCAGATTGCTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProAsnCysGlnIleArg 656
QY 2010 TCAGATCTATGGCTGTGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
QY 2058 GTAGCTATACCAGCAGACTCCCTGAAAGCGCTACATTGAGAACATTTTACCATTCCAAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTCCTTCTTTTATTATTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATTGCTATATGTTGAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
QY 2232 TCAAGCGATGAGCAACTGAAAGTGAGAGTGAACTTAAAGGG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726
RESULT 14
AAQ89099 PRELIMINARY; PRT; 787 AA.
ID AAQ89099 PRELIMINARY; PRT; 787 AA.
AC AAQ89099; 27, Created
DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)
DE Similar to MDC family.
GN UNQ5982.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,


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Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
Qy 1899 TACTTG-----GTTTATGTTTACTACTGACAAATGCAATGATAGAGTGTATGC 1949
Db 618 IleIleIysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
Qy 1950 AATAACAAGAAGCACTGCTCACTGAGTGCCTTCAATTTACTCCAGATTCTCAGTTCAA 2009
Db 637 AspSerArgAsnIysCysHisCysSerProGlyTyrIysProProAsnCysGlnIleArg 656
Qy 2010 TCAGATCTATGGCTGCTGGAGTATT-----GACAGTGGCAATTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
Qy 2058 GTAGCTATACAGCCAGACCTCCCTGAAAGGCGTACATTGAGAACATTTACCATTCCAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
Qy 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTCTCTTTATTATTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
Qy 2172 CTGATTGCTATAATGGTGAAGATTAATTTCCAAAGGAAAAAATGGAGAACTGAGCACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysIleTyrPheAlaLysGlu--- 714
Qy 2232 TCAAGCATGAGCAACTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 15
Q8TC42 PRELIMINARY; PRT; 787 AA.
ID Q8TC42 AC Q8TC42
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A disintegrin and metalloprotease domain 32.
GN Name=ADAM32;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC026085; AAH26085.1; -.
DR HSSP; P30403; IN4Y.
DR MEROPS; M12_960; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR002870; Peptidase M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD00664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
KW Integrin; Metalloprotease; Protease.
SQ SEQUENCE 787 AA; 87931 MW; CE0F54A50466B336 CRC64;

Alignment Scores:
Pred. No.: 2,98e-106 Length: 787
Score: 1519.50 Matches: 309
Percent Similarity: 58.89% Conservative: 135
Best Local Similarity: 40.98% Mismatches: 259
Query Match: 31.68% Indels: 51
DB: 2 Gaps: 18

US-10-054-683-18 (1-2640) x Q8TC42 (1-787)
Qy 72 ATGTGGTCTTGTCTTCTGTCTGACGGGGCTCGGGGGCTCGGGATGAC---AGTAATTTT 128
Db 4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21
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Qy 480 CATGTAATTTACCAAGTAAACATAGAACAGAGATGTTTCTCTATATATATAGAGAGAT 539
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Job time : 559.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 10, 2005, 21:33:10 ; Search time 66 Seconds
(without alignments)
5305.440 Million cell updates/sec

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Searched: 478139 seqs, 66318000 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3984	83.1	734	5	PCT-US95-07295-8
3	3551	74.0	651	1	US-08-264-101-2
4	3551	74.0	651	2	US-08-765-243-2
5	3551	74.0	651	5	PCT-US95-07295-2
6	2440	50.9	735	2	US-08-765-243-6
7	2440	50.9	735	5	PCT-US95-07295-6
8	1512	31.5	457	1	US-08-264-101-4
9	1512	31.5	457	2	US-08-765-243-4
10	1512	31.5	457	5	PCT-US95-07295-4
11	1506.5	31.4	787	4	US-10-000-489-70
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13	951.5	19.8	790	4	US-10-140-002-204
14	949	19.8	722	4	US-09-617-145-2
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17	770.5	16.1	812	4	US-09-632-098-4
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19	767	16.0	849	4	US-09-548-797B-6
20	752.5	15.7	606	4	US-09-460-295B-12
21	740	15.4	832	4	US-09-634-252A-4
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45	665.5	13.9	540	4	US-09-786-256C-1

ALIGNMENTS

RESULT 1
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; Sequence 8, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids

Sequence 204, Appl
Sequence 2, Appli
Sequence 15, Appl
Sequence 32, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 12, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 10, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 18, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 14, Appl
Sequence 4, Appli
Sequence 1, Appli

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-243-8

Alignment Scores:

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Score: 3984.00 Matches: 734
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.07% Indels: 0
DB: 2 Gaps: 0

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Db 501 LysGluValGluPheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAspVal 520
QY 1632 TCTGGAACCTGTGTATAGTATGATTCAGGATACACAGATGTGAAGCTGACAAATCTGCAG 1691
Db 521 SerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeuGln 540
QY 1692 TGGGAAAATTAATATGTAATATGTAGTAAATTTTATTATCAAAATCCAGAGCCACT 1751
Db 541 CysGlyLysLeuIleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAlaThr 560
QY 1752 ATTATTTATGCCAATAAGTGACATCTCTGCATCTGTGGAAATTTGCCAGTGATCAT 1811
Db 561 IleIleTyrAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAspHis 580
QY 1812 GCAGACAGCCAAAGATGTGGATAAAAGATGGAACTTCTGTGGTTCAAAATAGGTTTGC 1871
Db 581 AlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysValCys 600
QY 1872 AGGATCAAGATGTGTAGTCTTCTACTACTGGTTATGATGTGCTACTACTGACAAATGC 1931
Db 601 ArgAsnGlnArgCysValSerSerTyrLeuGlyTyrAspCysThrThrAspLysCys 620
QY 1932 AATGATAGAGTGATGCAATAACAAAAGACACTGTCACTGTAGTGTCTCATATTTACCT 1991
Db 621 AsnAspArgGlyValCysAsnAsnLysIleHisCysHisCysSerAlaSerTyrLeuPro 640
QY 1992 CCAGATTGCTCAGTTCAATCAGATCTATGGCTGTGGAGTATGTACAGTGGCAATTTT 2051
Db 641 ProAspCysSerValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAsnPhe 660
QY 2052 CCACCTGTAGTATACAGCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACAT 2111
Db 661 ProProValAlaIleProAlaArgLeuProGluArgTyrIleGluAsnIleTyrHis 680
QY 2112 TCCAAACCAATGAGATGGCAATTTTCTTATTCACTCTCTTCTTATTATTCTGTGTA 2171
Db 681 SerLysProMetArgTrpProPhePheLeuPheIleProPheIlePheCysVal 700
QY 2172 CTGATTCCTATAATGGTGAAGTTTAATTTCCAAAGGAAAAAATGAGAACTGAGGACTAT 2231
Db 701 LeuIleAlaIleMetValLysValAsnPheGlnArgLysLysTrpArgThrGluAspTyr 720
QY 2232 TCAAGCGATGAGCACTGAAAGTGAGAGTGAACTAAAGG 2273
Db 721 SerSerAspGluGlnProGluSerGluSerGluProLysGly 734
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RESULT 3

US-08-264-101-2

; Sequence 2, Application US/08264101

; Patent No. 5693496

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GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,101
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-264-101-2
```

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Alignment Scores:
Pred. No.: 0 Length: 651
Score: 3551.00 Matches: 650
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.04% Indels: 0
DB: 1 Gaps: 0
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US-10-054-683-18 (1-2640) x US-08-264-101-2 (1-651)

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QY 324 CAAGATTTTCAGAAATTTTCGCCACTACCAAGGGTATATTGAAGTTATCCAAATCTGTG 383
Db 2 GlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGlyTyrProLysSerVal 21
QY 384 GTGATGGTTAGCATGTACTGGACTCAGGGGGTACTACAGTTTGAAAATGTTAGTTAT 443
Db 22 ValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGluAsnValSerTyr 41
QY 444 GGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTTCAACATCTAATTTTACCAAGTAAACAT 503
Db 42 GlyIleGluProLeuGluSerSerValGlyPheGluHisValIleTyrGlnValLysHis 61
QY 504 AAGAAAGCAGATGTTTCTTTATATATGAGAAGATATTGAATCAAGAGATCTGTCTTTT 563
Db 62 LysLysAlaAspValSerLeuTyrAsnGluLysAspIleGluSerArgAspLeuSerPhe 81
QY 564 AAATTACAAGCCGACAGCCACAGAGATTTTGCAGAAATATATAGAAATGCATGTTTATA 623
Db 82 LysLeuGlnSerAlaGluProGlnGlnAspPheAlaLysTyrIleGluMetHisValIle 101
QY 624 GTTGAAAAACAATGTATATATCATATGCGGTCTGTACACACTGTGTGCTCAAAAAGTT 683
Db 102 ValGluLysGlnLeuTyrAsnHisMetGlySerAspThrThrValValAlaGlnLysVal 121
QY 684 TTCAGTTGATTGGATTGACGAATGCTATTTTGTTCATTATTAATTATTAATTATTCGTG 743
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Db 122 PheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAsnIleThrIleIleLeu 141
Qy 744 TCCTTCATTGGAGCTTTGGATAGATGAAATAAATTCGAACCTCGGAGAGCTAAATCAG 803
Db 142 SerSerLeuGluLeuTrrIleAspGluAsnLysIleAlaThrThrGlyGluAlaAsnGlu 161
Qy 804 TTATTACACACATTTTAAAGATGAAACATCTTATCTTGTTTACGTCTCATGATGTG 863
Db 162 LeuLeuHisThrPheLeuArgTrpLysThrSerTyrLeuValLeuArgProHisAspVal 181
Qy 864 GCATTTTACTGTGTTACAGAGAAAGTCAAAATATGTTGTGCAACCTTTCAGAGGAG 923
Db 182 AlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAlaThrPheGlnGlyLys 201
Qy 924 ATGTGTGATGCAAACTATGACAGAGGTGTTGTTCTGCACCCAGAACCATTAAGTCTGAA 983
Db 202 MetCysAspAlaAsnTyrAlaGlyValValLeuHisProArgThrIleSerLeuGlu 221
Qy 984 TCATTGCGAGTTATTTAGCTCAATTAATGAGCCCTTAGTATGGGATCACTTATGATGAC 1043
Db 222 SerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyIleThrTyrAspAsp 241
Qy 1044 ATTAACAAATGCCAGTCTCAGGAGCTCTGCTGATTAATGATCCAGAGCAATTCATTTC 1103
Db 242 IleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnProGluAlaIleHisPhe 261
Qy 1104 AGTGGTGTGAAGATCTTTAGTAACCTGACGAGCTTCAAGACTTTGCACATTTTATTTCAAAG 1163
Db 262 SerGlyValLysIlePheSerAsnCysSerPheGluAspPheAlaHisPheIleSerLys 281
Qy 1164 CAGAGTCCAGTGTCTTCAATCAGCTCGCTTACATCTTTTCAACAGCAAGCA 1223
Db 282 GlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPhePheLysGlnGlnAla 301
Qy 1224 GTGTGTGTAATGCAAGCTGAGAGGAGGAGAGTGTGACTGTGGACTGACAGAT 1283
Db 302 ValCysGlyAsnAlaLysLeuGluAlaGlyGluCysAspCysGlyThrGluGlnAsp 321
Qy 1284 TGTGCTCTTATTTGAGAAACATGCTGTGATATGCCACATGTAGATTTAAAGCCGGTTCA 1343
Db 322 CysAlaLeuIleGlyGluThrCysCysAspIleAlaThrCysArgPheLysAlaGlySer 341
Qy 1344 AACTGTCTGAAGACCATCTGCGAAACTGCTTATTTATGTCAAAAGAAAGATGTGT 1403
Db 342 AsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSerLysGluArgMetCys 361
Qy 1404 AGGCTTCTTGAAGATGGACCTCCCTGAATATTGCAATGGATCATCTGCATCATGC 1463
Db 362 ArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGlySerSerAlaSerCys 381
Qy 1464 CCAGAAACCACTATGTTACAGCTGGGCATCCGTTGGACTGAATCAATGATCTGTATA 1523
Db 382 ProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsnGlnTrrIleCysIle 401
Qy 1524 GATGAGCTTTCTATGAGTGGGATGAAACATATGTACAGACACATTTGGCAAGAGTAGAG 1583
Db 402 AspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPheGlyLysGluValGlu 421
Qy 1584 TTTGGCCCTTCAGATGTTATTTACCTTAATTCAGAGCTGATGTATCTGGAACTGT 1643
Db 422 PheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAspValSerGlyAsnCys 441
Qy 1644 GGTATAGTATTGATGAGATACACAGCTGTGAAGCTGCACATCTGCAGTGGGAAATTA 1703
Db 442 GlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeuGlnCysGlyLysLeu 461
Qy 1704 ATATGTAATATGATGAGTAAATTTTATTATCAAAATTCAGAGCCATTTATTTATGCC 1763
Db 462 IleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAlaThrIleIleTyrAla 481
Qy 1764 AACATAAGTGACATCTCTGATGCTGTGGAATTTGCCAGTATCATGACAGCCAA 1823

Db 482 AsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAspHisAlaAspSerGln 501
Qy 1824 AAGATGTGGATAAAGATGGAACCTTCTTGTGGTTCAATTAAGGTTTGAGGAATCAAGA 1883
Db 502 LysMetTrrIleLysAspGlyThrSerCysGlySerAsnLysValCysArgAsnGlnArg 521
Qy 1884 TGTGTGAGTTCTTCATACCTTGGGTATGATGACTACTGACAAATGCAATGATAGAGGT 1943
Db 522 CysValSerSerTyrLeuGlyTyrAspCysThrThrAspLysCysAsnAspArgGly 541
Qy 1944 GTATGCAATTAACAAAAAGCACTGTCACTGTAGTCTTCAATTTTACCTCCAGATTGCTCA 2003
Db 542 ValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeuProProAspCysSer 561
Qy 2004 GTTCAATCAGATCTATGCGCTGTGGAGTATTACAGATGGCAATTTTCCACCTGTAGCT 2063
Db 562 ValGlnSerAspLeuTrrProGlyGlySerIleAspSerGlyAsnPheProProValAla 581
Qy 2064 ATACCAGCAGACTCCCTGAAAGCGCTACATTGAGAACATTTTACCATTCACAAACCAATG 2123
Db 582 IleProAlaArgLeuProGluArgTyrIleGluAsnIleTyrHisSerLysProMet 601
Qy 2124 AGATGGCCATTTTCTTATTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2183
Db 602 ArgTrrProPhePheLeuPheIleProPhePheIlePheCysValLeuIleAlaIle 621
Qy 2184 ATGTGAAAGTTAATTTCCAAAGAAAAATGGAGAACTGAGGACTATTCAAGCGATGAG 2243
Db 622 MetValLysValAsnPheGlnArgLysLysTrpArgThrGluAspTyrSerSerAspGlu 641
Qy 2244 CAACCTGAAAGTGAGAGTGAACTAAAGGG 2273
Db 642 GlnProGluSerGluSerGluProLysGly 651

RESULT 4
US-08-765-243-2
; Sequence 2, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APOLLINA
; STREET: P. O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-765-243-2

Alignment Scores:

Pred. No.:	0	Length:	651
Score:	3551.00	Matches:	650
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	74.04%	Indels:	0
DB:	2	Gaps:	0

US-10-054-683-18 (1-2640) x US-08-765-243-2 (1-651)

QY	324	CAAGATTTCAGAAATTTCTGCACCTACCAAGGGTATATTGAAGGTATCCAAAATCTGTG	383
DB	2	GlnAspPheGlnAenPheCysHisTyrGlnGlyTyrIleGluGlyTyrProLysSerVal	21
QY	384	GTGATGTTAGCAATGTAAGTACAGCTCAGGGGCTACTACAGTTGAAATGTTAGTTAT	443
DB	22	ValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGluAenValSerTyr	41
QY	444	GGATAGAACCCCTGGAGTCTTCAGTTGGCTTGAACATGTAATTTACCAAGTAAACAT	503
DB	42	GlyIleGluProLeuGluSerSerValGlyPheGluHisValIleTyrGlnValIleHis	61
QY	504	AAGAAAGCAGATGTTCTCTATATAATGAGAAGGATATTGAATCAAGAGATCTCTCTTT	563
DB	62	LysLysAlaAspValSerLeuTyrAsnGlnLysAspIleGluSerArgAspLeuSerPhe	81
QY	564	AAATTACAAAGCGCAGAGCCACACAAAGATTTTCAAGATATATAGAAATGCAATGATA	623
DB	82	LysLeuGlnSerAlaGluProGlnGlnAspPheAlaLysTyrIleGluMetHisValIle	101
QY	624	GTTGAAAACAAATGTAATCATATGGGCTCATACACTGTTGCGCTCAAAAAGTT	683
DB	102	ValGlnLysGlnLeuTyrAsnHisMetGlySerAspThrThrValAlaGlnLysVal	121
QY	684	TTCCAGTTGATTTGAAATGCAAAATGCTATTTTCTTCAATTAATATATACAAATATTCTG	743
DB	122	PheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAenIleThrIleLeu	141
QY	744	TCATTGAGGCTTTGGATAGATGAAATAAATGCAACCATCGAGAGCTTAATGAG	803
DB	142	SerSerLeuGluLeuTyrIleAspGluAenLysIleAlaThrThrGlyGluAlaAenGlu	161
QY	804	TTATTACACATTTTAAAGATGAAACATCTTATCTGTTTACCTCTCATGATGTG	863
DB	162	LeuLeuHisThrPheLeuA-gtrPlySerThrLeuValLeuArgProHisAspVal	181
QY	864	GCAITTTTACTTTTACAGAAAAAGTCAAAATATGTTGTGCAACCTTTTCAAGGGAAG	923
DB	182	AlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAlaThrPheGlnGlyLys	201
QY	924	ATGTGTGATGAAACTATGAGAGAGGTGTTGTTCTGCAACCCAGAACATAAGTCTGAA	983
DB	202	MetCysAspAlaAenTyrAlaGlyValValLeuHisProArgThrIleSerLeuGlu	221
QY	984	TCACCTTCAGTTATTTAGCTCAATATTGAGCCTTAGTATGGGATCACTTATGATGAC	1043
DB	222	SerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyIleThrTyrAspAsp	241
QY	1044	ATTAACAAATGCCAGTCTCTCAGGAGCTGCTGCAATTAATGATCCAGAACAAATTCATTTC	1103
DB	242	IleAenLysCysGlnCysSerGlyAlaValCysIleMetAenProGluAlaIleHisPhe	261
QY	1104	AGTGGTGTGAAGATCTTTAGTAATCGCAGCTTCGAGACTTTGCAATTTTATTTCAAAG	1163
DB	262	SerGlyValLysIlePheSerAsnCysSerPheGluAspPheAlaHisPheIleSerLys	281
QY	1164	CAGAAGTCCCAGTCTCTTCAAAATCAGCCTCGCTTAGATCTCTTTTCAACACGACGCA	1223
DB	282	GlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPhePheLysGlnGlnAla	301

RESULT 5

QY	1224	GTGTGTGTAATGCAAAAGCTCGAAGCAGAGAGAGTGTGACTGTGTGGACTGAACAGGAT	1283
DB	302	ValCysGlyAenAlaLysLeuGluAlaGlyGluGluCysAspCysGlyThrGluGlnAsp	321
QY	1284	TGTGCCCTTATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTAAAGCCGGTTCA	1343
DB	322	CysAlaLeuIleGlyGluThrCysCysAspIleAlaThrCysArgPheLysAlaGlySer	341
QY	1344	AACTGTGCTCAAGGACCATGCTCGGAAAACCTGCTATTATTTATGTCAAAAGAAAGATCTGT	1403
DB	342	AsnCysAlaGluGlyProCysCysGluAenCysLeuPheMetSerLysGluArgMetCys	361
QY	1404	AGGCCTTCCCTTTGAAGAATCGACCTCCCTCAATATTGCAATGGATCATCTGCATCATGC	1463
DB	362	ArgProSerPheGluGluCysAspLeuProGluTyrCysAenGlySerSerAlaSerCys	381
QY	1464	CGAGAAAACCACTATGTTTCAAGCTGGGCATCCGTGTGGACTGAATCAATGATCTGTATA	1523
DB	382	ProGluAenHisTyrValGlnThrGlyHisProCysGlyLeuAenGlnTyrIleCysIle	401
QY	1524	GATGGAGTTTGTATGATGGGGATAAACAATGTACAGACACATTTGGCAAGAGTAGAG	1583
DB	402	AspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPheGlyLysGluValGlu	421
QY	1584	TTTGGCCCTTTCAGAAATGTTATTCTCACCTTAATTTCAAAGACTGATGTATCTGAAAACGT	1643
DB	422	PheGlyProSerGluCysTyrSerHisLeuAenSerLysThrAspValSerGlyAenCys	441
QY	1644	GGTATAGTGAATTCAGGATACACACAGTGTGAAGCTGACAAATCTGCAGTCGGGAAATTA	1703
DB	442	GlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAenLeuGlnCysGlyLysLeu	461
QY	1704	ATATGTAATATGTAGTAAATTTTATTACAAATTTCCAAAGCCACTATTATTATTATGCC	1763
DB	462	IleCysLysTyrValGlyLysPheLeuGlnIleProArgAlaThrIleIleTyrAla	481
QY	1764	AACATAAGTGCACATCTCTGCATTGCTGTGGAATTTGCCAGTGCATCATGCAGACAGCAA	1823
DB	482	AsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAspHisAlaAspSerGln	501
QY	1824	AGATGTGGATAAAGATGGAATCTTGTGGTTTCAATTAAGGTTTCAGGAATCAAGA	1883
DB	502	LysMetTrpIleLysAspGlyThrSerCysGlySerAenLysValCysArgAenGlnArg	521
QY	1884	TGTGTGAGTCTTTCATACCTTGGGTATGATTGTACTACTCACAATGCAATGATAGAGT	1943
DB	522	CysValSerSerSerTyrLeuGlyTyrAspCysThrThrAspLysCysAenAspArgGly	541
QY	1944	GTATGCAATAACAAAAGCACTGCTACTGTAGTGTCTTCAATATTACCTCCAGATTGCTCA	2003
DB	542	ValCysAenAenLysLysHisCysHisCysSerAlaSerTyrLeuProProAspCysSer	561
QY	2004	GTTCAATCAGATCTATGGCTGTGGAGTATTGACAGTGGCAATTTCCACCTGTAGCT	2063
DB	562	ValGlnSerAspLeuTrpProGlyGlySerIleAspSerGlyAenPheProProValAla	581
QY	2064	ATACCAAGCAGACTCCCTGAAAGCGCTACATTGAGAACATTTTACCATTCCAAACCAATG	2123
DB	582	IleProAlaArgLeuProGluArgTyrIleGluAenLysIleHisSerLysProMet	601
QY	2124	AGATGGCCATTTTCTTATTTCATTTCTCTTCTTATTATTATTCTGTGACTGATGCTATA	2183
DB	602	ArgTrpProPhePheLeuPheIleProPhePheIlePheCysValLeuIleAlaIle	621
QY	2184	ATGGTGAAGTTAATTTCCAAAGGAAAAATGAGAACTGAGGACTATTTCAGGAGTAG	2243
DB	622	MetValLysValAenPheGlnArgLysLysTrpArgThrGluAspTyrSerSerAspGlu	641
QY	2244	CAACCTGAAAGTCAGAGTAGTAACCTAAAGGG	2273
DB	642	GlnProGluSerGluSerGluProLysGly	651


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PCT-US95-07295-2
; Sequence 2, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07295-2

Alignment Scores:
Pred. No.: 0 Length: 651
Score: 3551.00 Matches: 650
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.04% Indels: 0
DB: 5 Gaps: 0

US-10-054-683-18 (1-2640) x PCT-US95-07295-2 (1-651)

QY 324 CAAGATTTTCAGAAATTTCTGCCACTACCAAGGGTATATTGAAGGTATCCAAATCTGTG 383
DB 2 GlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGlyTyrProLysSerVal 21
QY 384 GTGATGTTAGCATGTACTCGGACTCAGGGGGGTACTACAGATTTGAAAATGTTAGTTAT 443
DB 22 ValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGluAsnValSerTyr 41
QY 444 GGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGCAACATGTAATTACCAAGTAAACAT 503
DB 42 GlyIleGluProLeuGluSerSerValGlyPheGluHisValIleTyrGlnValLysHis 61
QY 504 AAGAAAGCAGATGTTCTCTATATATGAGAAGGATATTGAATCAGAGATCTGCTCTTT 563
DB 62 LysLysAlaAspValSerLeuTyrAsnGluLysAspIleGluSerArgAspLeuSerPhe 81
QY 564 AAATTACAAAGCCGACAGCCACAGCAAGATTTTGCAAGATATATAGAAATGCATGTTATA 623
DB 82 LysLeuGlnSerAlaGluProGlnGlnAspPheAlaLysTyrIleGluMetHisValIle 101
QY 624 GTTGAAAAACAATGTATATCATATGGGGTCTGATACAACTGTGTGCTCAAAAAGTT 683
DB 102 ValGluLysGlnLeuTyrAsnHisMetGlySerAspThrThrValValAlaGlnLysVal 121

684 TTCAGTTGATGGATTGACGAATGCTATTTTGTGTTTCAATTAATATTACAAATTTATTCTG 743
122 PheGlnLeuIleGlyLeuThrAsnAlaIlePheValSerPheAsnIleThrIleIleLeu 141
744 TCTTCATTGGAGCTTTGGATAGATGAAATAAAATTCGAACCACTGAGAGAAGCTAATGAG 803
142 SerSerLeuGluLeuTyrIleAspGluAsnLysIleAlaThrThrGlyGluAlaAsnGlu 161
804 TTATTACACACATTTTAAAGTGAACATCTTATCTGTTTACCTCTCATGATGATG 863
162 LeuLeuHisThrPheLeuArgTyrPheThrSerTyrLeuValLeuArgProHisAspVal 181
864 GCATTTTACTGTTTACAGAGAAAAGTCAAAATATGTTGTTGCAACCTTTTCAAGGGAAG 923
182 AlaPheLeuLeuValTyrArgGluLysSerAsnTyrValGlyAlaThrPheGlnGlyLys 201
924 ATGTGTGATGCAAACTATGAGAGAGGTGTTGTTCTGCACCCCAAGAACATTAAGTCTGAA 983
202 MetCysAspAlaAsnTyrAlaGlyGlyValValLeuHisProArgThrIleSerLeuGlu 221
984 TCACCTTGACGTATTTTAGCTCAATTTATGAGCCTTAGTATGGGATCACATTATGATGAC 1043
222 SerLeuAlaValIleLeuAlaGlnLeuLeuSerLeuSerMetGlyIleThrTyrAspAsp 241
1044 ATTAACAAATGCCAGTGCTCAGGAGCTGCTGCATTTATGAATCCAGAAGCAATTCATTTTC 1103
242 IleAsnLysCysGlnCysSerGlyAlaValCysIleMetAsnProGluAlaIleHisPhe 261
1104 AGTGTGTGAAGATCTTTTAGTAACTGCGAGCTTCGAAGACTTTGACATTTTATTTCAAAG 1163
262 SerGlyValLysIlePheSerAsnCysSerPheGluAspPheAlaHisPheIleSerLys 281
1164 CAGAAGTCCCAGTGTCTTCACAATAGCCCTCGCTAGATCCTTTTCAAACAGCAAGCA 1223
282 GlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspProPheLysGlnGlnAla 301
1224 GTGTGTGTAATGCAAGCTTGAAGCAGGAGAGAGTGTGACTGTGGAGCTGAACAGGAT 1283
302 ValCysGlyAsnAlaLysLeuGluAlaGlyGluCysAspCysGlyThrGluGlnAsp 321
1284 TGTGCCCTTATTCGAGAAACATGCTGTGATATTGCCACATGTAGATTTAAAGCGGTTCA 1343
322 CysAlaLeuIleGlyGluThrCysCysAspIleAlaThrCysArgPheLysAlaGlySer 341
1344 AACTGTGCTGAAGGACCATGCTCGGAAACTGTCTATTATGTCARAAAGAAAGATCTGT 1403
342 AsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSerLysGluArgMetCys 361
1404 AGCCCTTCTTCAAGAAATCGGACCTCCCTGGAATATTGCAATGGATCATCTGCATCATGC 1463
362 ArgProSerPheGlnGluCysAspLeuProGluTyrCysAsnGlySerSerAlaSerCys 381
1464 CCAGAAAACCACTATGTTACAGACTGGGCATPCCTGTGGACTGAATCAATGATCTGATA 1523
382 ProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsnGlnTyrIleCysIle 401
1524 GATGGAGTTGTATGATGGGGATAAACATGTACAGACACATTTGSCAAAGAAGTAGAG 1583
402 AspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPheGlyLysGluValGlu 421
1584 TTTGGCCCTTCAGAATGTTATCTCACCTTAATTTCAAAGACTGATGTATCTGGAACCTGT 1643
422 PheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAspValSerGlyAsnCys 441
1644 GGTATAAGTGATTTCAGGATACACAGATGTGAAGCTGACAAATCTGCAGTGGGAAAAATTA 1703
442 GlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeuGlnCysGlyLysLeu 461
1704 ATATGTAATATGATAGGTAAATTTTATTACAAATTTCCAAAGACCACTATTATTATGCC 1763
462 IleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAlaThrIleIleTyrAla 481
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QY 1764 AACATAAGTGCACATCTCTGCGATTCGTGGAATTTGCCAGTGTATCATGCGAGACAGCAA 1823
Db 482 AsnIleSerGlyHisLeuCySileAlaValGluPheAlaSerAspHisAlaAspSerGln 501
QY 1824 AAGATGTGGATAAAGATGAACACTCTTGTGGTTCAAAATAAGGTTTCAGGAATCAAGA 1883
Db 502 LysMetIrpIleLysAspGlyThrSerCySglySerAsnLysValCySA-gAsnGlnArg 521
QY 1884 TGTGTGAGTCTTCATACACTTGGGGTATGATTTGACTACTGACAAATGCAATGATAGAGGT 1943
Db 522 CyValSerSerSerTyrLeuGlyTyrAspCySethrThrAspLysCySAsnAspArgGly 541
QY 1944 GTATGCAATACAAAAAGCACTGTCACCTAGTGTCTTCATATTTACCTCCAGATTGCTCA 2003
Db 542 ValCySAsnAsnLysHisCySHisCySAsrAlaSerTyrLeuProProAspCySAsr 561
QY 2004 GTTCAATCAGATCTATCGCTGTGGGAGTATTCACAGTGGCAATTTCCACCTGTAGCT 2063
Db 562 ValGlnSerAspLeuIrpProGlyGlySerIleAspSerGlyAsnPhrProProValAla 581
QY 2064 ATACCAAGCCAGACTCCCTGAAAGCGCTACATTCAGAACATTTACCAATTCACAAACCAATG 2123
Db 582 IleProAlaArgLeuProGluArgArgTyrIleGluAsnIleTyrHisSerLysProMet 601
QY 2124 AGATGGCCATTTTCTTATTCATCTCTTCTTATTTATTTATTTCTGTGTACTGCTATA 2183
Db 602 ArgTrpProPhePheLeuPheIleProPhePheIleIlePheCysValLeuIleAlaIle 621
QY 2184 ATGGTGAAGCTTAATTTCCAAAGGAAAAATGGAGACTGAGGACTATTCAGCGATGAG 2243
Db 622 MetValLysValAsnPheGlnArgLysLysLysLysLysLysLysLysLysLysLysLys 641
QY 2244 CAACCTGAAAGTGCAGAGTGAACCTTAAAGGG 2273
Db 642 GlnProGluSerGluSerGluProLysGly 651

RESULT 6
US-08-765-243-6
; Sequence 6, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLI, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-243-6

Alignment Scores:
Pred. No.: 7,98e-222 Length: 735
Score: 2440.00 Matches: 439
Percent Similarity: 75.71% Conservative: 119
Best Local Similarity: 59.57% Mismatches: 167
Query Match: 50.88% Indels: 12
DB: 2 Gaps: 7

US-10-054-683-18 (1-2640) x US-08-765-243-6 (1-735)
QY 78 GTCTGTGTTCTGCTCAGCGGG-----CTCGGGGGGCTG-----CGATGGAC 119
Db 4 IleLeuLeuLeuLeuSerGlyLeuSerGluLeuGlyGlyLeuSerGlnSerGlnThrGlu 23
QY 120 AGTAATTTGATAGTTTACCTGCTGCAAAATTACAGTTCCGAGAGAAATACGGTCAATAA 179
Db 24 GlyThrArgGluLysLeuHisValGlnValThrValProGluLysIleArgSerValThr 43
QY 180 AAGGAAGGAATTCAATCGCAGGCATCTACAAAATTGTAATTCAGAGGAAACCATATACT 239
Db 44 SerAsnGlyTyrGlnThrGlnValThrTyrAsnLeuLysIleGluGlyLysThrTyrThr 63
QY 240 GTCAATTTAATGCAAAAAAACTTTTACCCCATTAATTTAGAGTTTACAGTTATAGTGGC 299
Db 64 LeuAspLeuMetGlnLysProPheLeuProAsnPheArgValTyrSerTyrAspAsn 83
QY 300 ACAGGAATATGAACACCTGACCAAGATTTCAGAAATTTCCGCACCTACCAAGGATAT 359
Db 84 AlaGlyIleMetArgSerLeuGluGlnLysPheGlnAsnIleCysTyrPheGlnGlyTyr 103
QY 360 ATTGAAGGTTATCCAAAATCTGTTGGTGTAGTGTAGCACATGTACTGACCTCAGGGCGTA 419
Db 104 IleGluGlyTyrProAsnSerMetValIleValSerThrCysThrGlyLeuArgGlyPhe 123
QY 420 CTACAGTTTGAAATGTTAGTTATGGAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAA 479
Db 124 LeuGlnPheGlyAsnValSerTyrGlyIleGluProLeuGluSerSerGlyPheGlu 143
QY 480 CATGTAATTTACCAAGTAAACATAGAAAGCAGATGTTTCCCTTATATATATAGAAAGAT 539
Db 144 HisValIleTyrGlnValGluProGluLysGlyGlyAlaLeuLeuTyrAlaGluLysAsp 163
QY 540 ATTGAATCAGAGATCTGCTCTTTAAATATACAAAGCGCAGACGACAGCAAGATTTTGCA 599
Db 164 IleAspLeuArgAspSerGlnTyrLysIleArgSerIleLysProGlnArgIleValSer 183
QY 600 AAGTATATAGAAATGCAATGTTATAGTTGAAAAACAATTTGATATATCATATGGGCTCTGAT 659
Db 184 HisTyrLeuGluIleHisIleValValGluLysGlnMetPheGluHisIleGlyAlaAsp 203
QY 660 ACACTGTTGCTGCTCAAAAGTTTCCAGTTGATGGATGAGCAATGCTATTTTGT 719
Db 204 ThrAlaIleValThrGlnLysIlePheGlnLeuIleGlyLeuAlaAsnAlaIlePheAla 223
QY 720 TCATTAAATATTAATTTCTGCTCTTCAATTCGAGCTTTGGATAGATGAAAAATAAAT 779
Db 224 ProPheAsnLeuThrValIleLeuSerSerLeuGluPheTrpMetAspGluAsnLysIle 243
QY 780 GCAACCACTGGAGAAGCTAATAGTTTATTACACACATTTTAAAGATGGAACATCTTAT 839
Db 244 LeuThrThrGlyAspAlaAsnLysLeuLeuTyrArgPheLeuLysTyrLysGlnSerTyr 263
QY 840 CTTGTTTACGCTCCTCATGATGCGCATTTTCTGTTTACAGAGAAAGTCAATATAT 899
Db 264 LeuValLeuArgProHisAspMetAlaPheLeuLeuValTyrArgAsnThrThrAspTyr 283
QY 900 GTTGGTGAACCTTTCAAGGGAAGATGTGTGATGCAACCTATTCAGGAGGTGTGTCTG 959
Db 284 ValGlyAlaThrTyrGlnGlyLysMetCysAspLysAsnTyrAlaGlyValAlaLeu 303
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QY	180	AAGGAAGCAAT	TGAATCGCAGGCAT	CCTCAAAAAT	TGTAATTCGAAGGAAA	CCATATACT	239
DB	44	SerAsnGly	TyrGluThrGlnVal	ThrTyrAsnLeu	lysIleGluGly	ysThrTyrThr	63
QY	240	GTGAATTAAT	GCAGAAAAA	ACTTTTACC	CCATAATTTAGAGTTTACAGTTATAGTGC	299	
DB	64	LeuAspLeu	MetGlnLys	ProPheLeu	ProAsnPheArg	ValTyrSerTyrAspAsn	83
QY	300	ACAGGAATTAT	GAACACAC	TGTGACCA	AGATTTTCAGAA	TTTCTGCCACTACCAAGGAT	359
DB	84	AlaGlyIle	MetArgSerLeu	GluGlnLys	PheGlnAsn	IleCysTyrPheGlnGlyTyr	103
QY	360	ATTGAAGGTT	ATCCAAAAT	CTGTGGT	AGTGGTTAGACACAT	GTACTGGAGTTCAGGGCGCTA	419
DB	104	IleGluGly	TyrProAsnSer	MetValIle	ValSerThrCys	ThrGlyLeuArgGlyPhe	123
QY	420	CTACAGTTT	GAAAATG	TTAGTTAG	GAATAGAACCCCTGGAGTCTTCAGTTGGCTTTGAA	479	
DB	124	LeuGlnPhe	GlyAsnValSer	TyrGlyIle	GluProLeuGlu	SerSerGlyPheGlu	143
QY	480	CATGTAATTT	ACCAGTAATA	ACATAACAA	AGCAGAGATGTTTCTTATATA	TATAGAGAAGGAT	539
DB	144	HisValIle	TyrGlnValGlu	ProGluGly	serGlyAlaLeu	LeuTyrAlaGluLysAsp	163
QY	540	ATTGAATCA	AGAGATCT	GTCTCTT	TAATAATCA	AAAGCGCAGCACGACGAAAGTTTGC	599
DB	164	IleAspLeu	ArgAspSerGln	TyrLysIle	ArgSerIleLys	ProGlnArgIleValSer	183
QY	600	AAGTATAT	AGAAATGC	ATGTATAG	TTGAAAACAA	CAATGTATATCATATGGGGCTGAT	659
DB	184	HisTyrLeu	GluIleHisIle	ValValGlu	LysGlnMetPhe	GluHisIleGlyAlaAsp	203
QY	660	ACAACTGTT	GCCTCAAAA	AGTTTCCAGT	TGATTCGATTGACGAATGCTATTTTGT	719	
DB	204	ThrAlaIle	ValThrGlnLys	IlePheGln	LeuIleGlyLeu	AlaIlePheAla	223
QY	720	TCATTTAAT	ATACAA	TATTTCTCT	CTTCATTTGGAGCTTTGGAT	PAGATGAAAATAAAAT	779
DB	224	ProPheAsn	LeuThrValIle	LeuSerSerLeu	GluPheTrpMetAsp	GluAsnLysIle	243
QY	780	GCACCACT	GGAGAGCT	TAATGAGT	TATTACACACATTTT	TNAGATGGAAAACATCTTAT	839
DB	244	LeuThrThr	GlyAspAlaAsn	LysLeuLeu	TyrArgPheLeu	lysTrpLysGlnSerTyr	263
QY	840	CTTGTTT	TACGCTCAT	GTGCGCAT	TTTTTACTTGTTTACAGAGAAA	AGTCAAATTAT	899
DB	264	LeuValLeu	ArgProHisAsp	MetAlaPhe	LeuLeuValTyrArgAsn	ThrThrAspTyr	283
QY	900	GTTGGT	GCAACTT	TCAAGG	AGAGTGTGATGC	CAAACTATGACAGAGGTGTGTTCTG	959
DB	284	ValGlyAla	ThrTyrGln	GlyLysMetCys	AspLysAsnTyrAla	GlyValAlaLeu	303
QY	960	CACCCGAGA	ACCATAA	GTCTCGAAT	CACTTCAGTATTTT	TAGCTCAATATTATGAGCCTT	1019
DB	304	HisProLys	AlaValThrLeu	GluSerLeu	AlaIleIleLeuVal	GlnLeuLeuSerLeu	323
QY	1020	AGTATGGG	AGTACCTT	ATGATGAC	ATTAACAAA	TGCCAGTGCTCAGGAGCTGTGTCAT	1079
DB	324	SerMetGly	LeuAlaTyrAsp	AspValAsn	LysCysGlnCys	GlyValProValCysVal	343
QY	1080	ATGAATCC	AGAAGCA	ATTCA	TTTCAGTGGTGTGA	AGATCTTTAGTAACTCGCAGCTTCGAA	1139
DB	344	MetAsnPro	GluAlaProHis	SerSerGly	ValArgAlaPheSer	AsnCysSerMetGlu	363
QY	1140	GACTTTG	CACATTTT	ATTTTCAA	AGCAGAAGTCC	CAGTGTCTTCAATCAGCCTCGCTTA	1199
DB	364	AspPheSer	LysPheIle	ThrSerGln	SerSerHisCys	LeuGlnAsnGlnProThrLeu	383
QY	1200	GATCCTTT	TTTCAA	ACAGCA	GCAGTGTGTG	TGTAATGCAAAAGCTGGAGCAGGAGAG	1259
DB	384	GlnProSer	TyrLys---	MetAla	ValCysGlyAsn	GlyGlyValGluGluAspGluIle	402

1260	QY	TGTGACTGTGGGACTGAACAGGATTGTGCCCTTATTATGGAGAAACATGCTGTGTGATATGGC	1311
403	DB	CysAspCysGly---LysLysGlyCysAlaGluMetProProCysCysAsnProAsp	421
1320	QY	ACATGTAGATTTAAAGCCGGTTCAAACCTGTGCTGAAGGACCATGCTGCGAAAACTGTCTTA	1379
422	DB	ThrCysLysLeuSerAspGlySerGluCysSerSerGlyIleCysCysAsnSerCysLys	441
1380	QY	TTTATGTCAAAGAAGAAGATGTGTAGGCCCTTCCTTTGAAGAATGCGACCTCCCTGAAATAT	1439
442	DB	LeuLysArgLysGlyGluValCysArgLeuAlaGlnAspGluCysAspValThrGluTyr	461
1440	QY	TGCAATCGATCATCTGCATCATGCCAGAAAAACCACATATGTTTCAGACTGGGCATCCCGTGT	1499
462	DB	CysAsnGlyThrSerGluValCys---GluAspPheValGlnAsnGlyHisProCys	480
1500	QY	GGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATAGTGGGATAAACAATGTACA	1559
481	DB	AspAsnArgLysTrpIleCysIleAsnGlyThrCysGlnSerGlyGluGlnGlnCysGln	500
1560	QY	GACACATTTGCAAGAGTAGAGCTTTGGCCCTTCAGAATGTTTATCTCACCTTAATATCA	1619
501	DB	AspLeuPheGlyIleAspAlaGlyPheGlySerSerGluCysPheTrpGluLeuAsnSer	520
1620	QY	AAGACTGATGTATCTGAAAACCTGTGTATAGTGATTCAGAGATACACACATGTGAAGCT	1679
521	DB	LysSerAspIleSerGlySerCysGlyIleSerAlaGlyGlyTrpLysGluCysProPro	540
1680	QY	GACAATCTGCAGTCGGGAAAATTAATATGTAAATATCTAGGTAATTTTATTATACAAAT	1739
541	DB	AsnAspArgMetCysGlyLysIleIleCysLysTrpGlnSerGluAsnIleLeuLysLeu	560
1740	QY	CCAAGAGCCACTATTATTATGCCAACATAGTGGAATCTCTGCATTTGCTGTGGAATTT	1799
561	DB	ArgSerAlaThrValIleTyrAlaAsnIleSerGlyHisValCysValSerLeuGluTyr	580
1800	QY	GCCAGTGATCATGCAGACAGCCAAAGATGTGGAATAAAGATGAACCTCTTGTGGTTCA	1859
581	DB	ProGlnGlyHisAsnGluSerGlnLysMetTrpValArgAspGlyThrValCysGlySer	600
1860	QY	AATAAGGTTTTCAGGAATCAAGATGTGTAGGTTCTTCATACTTGGGTATGATGTACT	1919
601	DB	AsnLysValCysGlnAsnGlnLysCysValAlaAspThrPheLeuGlyTyrAspCysAsn	620
1920	QY	ACTGACAAATCCAATGATAGAGGTGTATGCAATTAACAAAAGCATGTCACTGTAGTGCT	1979
621	DB	LeuGluLysCysAsnHisHisGlyValCysAsnAsnLysLysAsnCysHisCysAspPro	640
1980	QY	TCATATTTACCTCCAGATTGCTCAGTTCAATCAGATCATGGCTGTGGGAGTATTGAC	2039
641	DB	ThrTyrLeuProProAspCysLysArgMetLysAspSerTyrProGlyGlySerIleAsp	660
2040	QY	AGTGGCAATTTCCACCTGTAGCTTATACCACCCAGACTCCCTGAAAGCGCTACATTGAG	2099
661	DB	SerGlyAsn---LysGluArgAlaGluPro-----IleProValArgProTyrIleAla	677
2100	QY	AACATTTTACCATTCCAAACCAATCAGATGGCCATTTTCTTATTCAATCTCTTTTATT	2159
678	DB	SerArgTyrArgSerLysSerProArgTrpProPhePheLeuIleIleProPheTyrVal	697
2160	QY	ATTTTCTGTGTACTGATGTCTTAATGTGTGAAGTTAATTTCCAAAGGAAAAATGGAGA	2219
698	DB	ValIleLeuValLeuIleGlyMetLeuValLysValTyrSerGlnArgMetLysTrpArg	717
2220	QY	ACTGAGGACTATTCAAGCGATCAGCAACCTGAAAGTGAGAGTGAACTTAAA	2270
718	DB	MetAsnAsnPheSerSerGluGluGlnPheGluSerGluSerGluSerLysLys	734

RESULT 8
US-08-264-101-4
; Sequence 4, Application US/08264101
; Patent No. 5693496
; GENERAL INFORMATION:

; APPLICANT: ALVES, KENNETH
 ; APPLICANT: GUPTA, SUNIL K.
 ; APPLICANT: HOLLIS, GREGORY F.
 ; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MARY A. APPOLLINA
 ; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 ; CITY: RAHWAY
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: US/08/264,101
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: APPOLLINA, MARY A.
 ; REGISTRATION NUMBER: 34,087
 ; REFERENCE/DOCKET NUMBER: 19244
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908)594-3462
 ; TELEFAX: (908)594-4720
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-264-101-4

Alignment Scores:

Pred. No.: 3,36e-134 Length: 457
 Score: 1512.00 Matches: 265
 Percent Similarity: 73.70% Conservative: 74
 Best Local Similarity: 57.61% Mismatches: 115
 Query Match: 31.53% Indels: 6
 DB: 1 Gaps: 5

US-10-054-683-18 (1-2640) x US-08-264-101-4 (1-457)

QY 891 TCAATATGTTGGTGAACCTTTCAAGGGAAGATGTTGATGCAAACTATGACGAGGT 950
 Db 3 SerAspTyrValGlyAlaThrTyrGlnGlyLysMetCysAspLysAsnTyrAlaGlyGly 22
 QY 951 GTTGTCTCGACCCCAAGCAACATAAGTCTGGAATCACTTCAGTATTTTAGCTCAATTA 1010
 Db 23 ValAlaLeuHisProLysAlaValThrLeuGluSerLeuAlaIleLeuValGlnLeu 42
 QY 1011 TTGACGCTTAGTATGGGATCACTTATGATGACATTAAACAAATGCCAGTCTCAGGAGCT 1070
 Db 43 LeuSerLeuSerMetGlyLeuAlaTyrAspValAsnLysCysGlnCysGlyValPro 62
 QY 1071 GTCTGCATTATGATCGAAGCAATTCATTTCAGTGGTGTGAAGATCTTTAGTAAGTGC 1130
 Db 63 ValCysValMetAsnProGluAlaProHisSerSerGlyValArgAlaPheSerAsnCys 82
 QY 1131 AGCTTCGAAGCTTTGCACATTTTATTCAAGCAGAGTCCAGTGTCTTTCACATCAG 1190
 Db 83 SerMetGluAspPheSerLysPheIleThrSerGlnSerSerHisCysLeuGlnAsnGln 102
 QY 1191 CCTCGCTTAGATCCTTTTTCAACACAGCAAGCTGTGTGTAATGCAAAAGCTGGAAGCA 1250
 Db 103 ProThrLeuGlnProSerTyrLys--MetAlaValCysGlyAsnGlyGluValGluGlu 121
 QY 1251 GGAAGAGAGTGTGACTGTGGACTGAACAGAGTATGTCCTTATTTGGAGAAACATGCTGT 1310
 Db 1251 GGAAGAGAGTGTGACTGTGGACTGAACAGAGTATGTCCTTATTTGGAGAAACATGCTGT 1310

RESULT 9

US-08-765-243-4
 ; Sequence 4, Application US/08765243
 ; Patent No. 5935578
 ; GENERAL INFORMATION:
 ; APPLICANT: ALVES, KENNETH
 ; APPLICANT: GUPTA, SUNIL K.

Db 122 AspGluIleCysAspCysGly---LysLysGlyCysAlaGluMetProProCysCys 140
 QY 1311 GATATTGCCACATGATGATTAAAGCGGTTCAAACTGTCTGAAGACCATGTGCGAA 1370
 Db 141 AsnProAspThrCysLysLeuSerAspGlySerGluCysSerSerGlyLleCysCysAsn 160
 QY 1371 AACTGTCTATTATGTCAAAGAAAGAAATGTGTAGGCTTCCTTTGAAGAAATGACCTC 1430
 Db 161 SerCysLysLeuLysArgLysGlyGluValCysArgLeuAlaGlnAspGluCysAspVal 180
 QY 1431 CCTGAATATTGCAATGATCATCTGCATCATGCCAGAAACACCACTATGTTACACATGGG 1490
 Db 181 ThrGluTyrCysAsnGlyThrSerGluValCys---GluAspPhePheValGlnAsnGly 199
 QY 1491 CATCCGTGTGGACTGAATCAATGATCTGTATAGATGGAGTTCGTATAGTGGGATATAA 1550
 Db 200 HisProCysAspAsnArgLysTrpIleCysIleAsnGlyThrCysGlnSerGlyGluGln 219
 QY 1551 CAATGTACACACATTTGGCAAGAGTAGAGTTTGGCCCTTCAGAAATGTTATTCTCAC 1610
 Db 220 GlnCysGlnAspLeuPheGlyLleAspAlaGlyPheGlySerSerGluCysPheTrpGlu 239
 QY 1611 CTTAAATTCGAAGACTGATGATCTGGAACCTGTGTATAGTATGATGATGATGATGATGAT 1670
 Db 240 LeuAsnSerLysSerAspIleSerGlySerGlyLleSerAlaGlyGlyTyrLysGlu 259
 QY 1671 TGTGAAGCTGACAACTGTCAGTGGGAAATTAATATGTAATATGATGATGATGATGATGAT 1730
 Db 260 CysProAsnAspArgMetCysGlyLysIleIleCysLysTyrGlnSerGluAsnIle 279
 QY 1731 TTCAAAATTCGAAGACTGATGATCTGGAACCTGTGTATAGTATGATGATGATGATGATGAT 1790
 Db 280 LeuLysLeuArgSerAlaThrValIleTyrAlaAsnIleSerGlyLleValCysValSer 299
 QY 1791 GTGGAATTTGCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1850
 Db 300 LeuGluTyrProGlnGlyHisAsnGluSerGlnLysMetTrpValArgAspGlyThrVal 319
 QY 1851 TGTGGTTTCAAAATGAAGTTTCGAGAAATCAAGATGTTGAGTGTCTTCTCATCTCTGGGTAT 1910
 Db 320 CysGlySerAsnLysValCysGlnAsnGlnLysCysValAlaAspThrPheLeuGlyTyr 339
 QY 1911 GATTGTACTACTGACAAATGCAATGATAGAGTGTATGCAATTAACAAAGACACTGCTCAC 1970
 Db 340 AspCysAsnLeuGluLysCysAsnHisGlyValCysAsnAsnLysLysAsnCysHis 359
 QY 1971 TGATGTCTCATATTTACCTCCAGATGTTGATGATGATGATGATGATGATGATGATGATGAT 2030
 Db 360 CysAspProThrTyrLeuProProAspCysLysArgMetLysAspSerTyrProGlyGly 379
 QY 2031 AGTATTGACAGTGGCAATTTTCCACCTGTAGCTATACCCAGCAGACTCCCTGAAAGCGC 2090
 Db 380 SerIleAspSerGlyAsn---LysGluArgAlaGluPro-----IleProValArgPro 396
 QY 2091 TACATTGAGAACAATTTACCAATCCAAACCAATGAGATGGCCATTTTCTTATTCTTCTCT 2150
 Db 397 TyrIleAlaSerArgTyrArgSerLysSerProArgTrpProPhePheLeuIlePro 416
 QY 2151 TTCTTTATTTTCTGTGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2210
 Db 417 PheTyrValValIleLeuValLeuIleGlyMetLeuValLysValTyrSerGlnArgMet 436
 QY 2211 AAATGAGAACTGAGGACTATTCAAGCGATGAGCAACTCAAAAGTGAAGTGAAGTGAAGTGAAG 2270
 Db 437 LysTrpArgMetAspAspPheSerSerGluGluGlnPheGluSerGluSerLys 456

Qy	1311	GATATTGCCACATGTAGATTAAAGCCGGTTCAAACTGTCTCTGAAGACCATCCTCGCAA	1370
Db	141	AsnProaspThrCysIysLeuSerAspGlySerGluCysSerGlyIleCysCysAsn	160
Qy	1371	AACTGTCTTATTTATGTCAAAAGAAAGAAATGTGTAGGCCTTCCTTTGAAGAATGCGACCTC	1430
Db	161	SerCysAluLeuIysArgIysGlyGluValCysArgLeuAlaGlnAspGluCysAspVal	180
Qy	1431	CTTGAAATATTGCAATGTGATCATCTGCATCATGATGCCCGAAGAAACCACTATTGTTCAGACTGGG	1490
Db	181	ThrGlnIyrCysAsnGlyThrSerGluValCys---GluAspPhePheValGlnAsnGly	199
Qy	1491	CATCCGTGTGGACTGAATCAATCGATCTGATAGATGGAGTGTGTGTAGCTGGGGATAAA	1550
Db	200	HisProCysAspAsnArgIysIleCysIleAsnGlyThrCysGlnSerGlyGluGln	219
Qy	1551	CAATGTACAGACACATTTGGCAAGAAGATAGACTTTGGCCCTTCAGAAATGTTATTCTCAC	1610
Db	220	GlnCysGlnAspLeuPheGlyIleAspAlaGlyPheGlySerSerGluCysPheTrpGlu	239
Qy	1611	CTTAATTCAAAGACTGATGTATCTGNAACATGTGGTATAGTGATTCAGACATCACACAG	1670
Db	240	LeuAsnSerIysSerAspIleSerGlySerCysGlyIleSerAlaGlyGlyIyrLysGlu	259
Qy	1671	TGTGAAGCTCACAACTCTGCAGTCGGGAAAATTAATATGTAAATATGTAGTAAATTTTA	1730
Db	260	CysProAsnAspArgMetCysGlyIysIleIleCysIysIyrGlnSerGluAsnIle	279
Qy	1731	TTACAAATTCAGAGACCATATTATTATTCGCAACATATAGTGAGCATCTCTGCATTGCT	1790
Db	280	LeuIysLeuArgSerAlaThrValIleIyrAlaAsnIleSerGlyIleValCysValSer	299
Qy	1791	GTGGAATTTGCCAGTATCATGCAGACAGCAAAAGATGTGGATATAAGATGGAACCTCT	1850
Db	300	LeuGlnIyrProGlnGlyHisAsnGluSerGlnIysMetIrpValArgAspGlyThrVal	319
Qy	1851	TGTGGTTTCAAATTAAGGTTTCAGGAATCAAAGATGTGTGAGTTCTTCATACTTGGGTTAT	1910
Db	320	CysGlySerAsnIysValCysGlnAsnGlnIysCysValAlaAspThrPheLeuGlyIyr	339
Qy	1911	GATTGTACTACTGACAAATCCATGATAGAGGTGTATGCAATACCAAAAGCACTGTCTAC	1970
Db	340	AspCysAsnLeuGlnIysCysAsnHisIleGlyValCysAsnAsnIysIysAsnCysHis	359
Qy	1971	TGTAGTCTTCATATTTACCTCCAGATTTGCTCAGTTCAATCAGATCTATGGCTGTGGG	2030
Db	360	CysAspProThrIyrLeuProProAspCysIysArgMetIysAspSerIyrProGlyGly	379
Qy	2031	AGTATTGACAGTGGCAATTTTCCACCTGTGTAGCTATACCAGCCAGACTCCCTGAAAGCGC	2090
Db	380	SerIleAspSerGlyAsn---LysGluArgAlaGluPro-----IleProValArgPro	396
Qy	2091	TACATTGAGAACATTTACCATTCCAACCAATCAGATGGCCATTTTCTTATTCTATTCTCT	2150
Db	397	TyrIleAlaSerArgIyrArgSerIysSerProArgIrpProPhePheLeuIleIlePro	416
Qy	2151	TTCTTTATTATTTCTGTACTGATGTCTPATTAATGTGAAAGTAATTTCCAAAGGAAA	2210
Db	417	PheIyrValValIleLeuValLeuIleGlyMetLeuValIysValIyrSerGlnArgMet	436
Qy	2211	AAATGGAGACTGAGGACTATTCAAGCGATGAGCAACCTGAAAGTGAGATGAACCTAAA	2270
Db	437	LysIrpArgMetAspPheSerSerGluGluGlnPheGluSerGluSerGluSerIys	456

RESULT 10

PCT-US95-07295-4

; Sequence 4, Application PC/TUS9507295

; GENERAL INFORMATION:

; APPLICANT: ALVES, KENNETH

; APPLICANT: GUPTA, SUNIL K.

; APPLICANT: HOLLIS, GREGORY F.

; TITLE OF INVENTION: CONTRACEPTIVE VACCINE

; NUMBER OF SEQUENCES: 8

US-10-054-683-18 (1-2640) x US-08-765-243-4 (1-457)

[illegible]

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MARY A. APOLLINA
 ; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 ; CITY: RAHWAY
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/07295
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: APOLLINA, MARY A
 ; REGISTRATION NUMBER: 34,087
 ; REFERENCE/DOCKET NUMBER: 19244Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908)594-3462
 ; TELEFAX: (908)594-4720
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-07295-4
 ;
 ; Alignment Scores:
 ; Pred. No.: 3,36e-134 Length: 457
 ; Score: 1512.00 Matches: 265
 ; Percent Similarity: 73.70% Conservative: 74
 ; Best Local Similarity: 57.61% Mismatches: 115
 ; Query Match: 31.53% Indels: 6
 ; DB: 5 Gaps: 5
 ;
 ; US-10-054-683-18 (1-2640) x PCT-US95-07295-4 (1-457)

QY 891 TCAAAATTTGTTGGTCAACCTTTCAAGGGAAGATGTGATGCAAACTATGCGAGGAGT 950
 Db 3 SerAspTyrValGlyAlaThrTyrGlnGlyMetCysAspLysAsnTyrAlaGlyGly 22
 QY 951 GTTGTCTGCAACCCCAACACATAGCTGGAATCACTTGCAGTATTATTTAGCTCAATTA 1010
 Db 23 ValAlaLeuHisProLysAlaValThrLeuGluSerLeuAlaIleLeuValGlnLeu 42
 QY 1011 TTGAGCCTTAGTATGGGGATCACTTATGATGACATTAACAAATGCCAGTGTCTCAGGAGCT 1070
 Db 43 LeuSerLeuSerMetGlyLeuAlaTyrAspAspValAsnLysCysGlnCysGlyValPro 62
 QY 1071 GTCTGCAATTATGATCAGAGCAATTCATTTCAGTGGTGTGAAGATCTTTAGTAATGTC 1130
 Db 63 ValCysValMetAsnProGluAlaProHisSerSerGlyValArgAlaPheSerAsnCys 82
 QY 1131 AGCTTCAAGACTTTGACATTTTATTTCAAGCAGAAGTCCCACTGCTCTTCACAATCAG 1190
 Db 83 SerMetGluAspPheSerLysPheIleThrSerGlnSerSerHisCysLeuGlnAsnGln 102
 QY 1191 CCTGCTTAGATCCTTTTCAACACAGCAAGCTGTGTGATGCAAAAGCTGGAAGCA 1250
 Db 103 ProThrLeuGlnProSerTyrLys--MetAlaValCysGlyAsnGlyGluValGluGlu 121
 QY 1251 GGAAGAGAGTGTACTGTGGGACTGAACAGAGTTGTGCCCTTATTTGAGAAACAGCTGT 1310
 Db 122 AspGluIleCysAspCysGly--LysLysGlyCysAlaGluMetProProCysCys 140
 QY 1311 GATATTGCCACATGATATTAAGCCGGTTCAAACTGCTGCTGAAGGACCATCTGCGAA 1370
 Db 141 AsnProAspThrCysLysLeuSerAspGlySerGluCysSerSerGlyIleCysCysAsn 160

QY 1371 AACTGTCTATTATGTCAAAGAAAGAAATGTGTAGGCTTCTCTTTGAAGAATGCGACCTC 1430
 Db 161 SerCysLysLeuLysArgLysGlyGluValCysArgLeuAlaGlnAspGluCysAspVal 180
 QY 1431 CCTGAATATTGCAATGATCATCTGCATCATGCCAGAAACCACTATGTTTCCAGCTGGG 1490
 Db 181 ThrGluTyrCysAsnGlyThrSerGluValCys--GluAspPheValGlnAsnGly 199
 QY 1491 CATCCGTGTGGACTGAATCAATGATCTGTATAGATGGAGTTTCTATGAGTGGGATATA 1550
 Db 200 HisProCysAspAsnArgLysTrpIleCysIleAsnGlyThrCysGlnSerGlyGluGln 219
 QY 1551 CAATGTACAGACATTTTGGCAAGAAGTAGAGTTTGGCCCTTCAGAAATGTTATTCTCAC 1610
 Db 220 GlnCysGlnAspLeuPheGlyIleAspAlaGlyPheGlySerSerGluCysPheTrpGlu 239
 QY 1611 CTTAATTTCAAAGACTGATGATCTGGAACCTGGTATAGTATAGTATCAGGATCACACAG 1670
 Db 240 LeuAsnSerLysSerAspIleSerGlySerCysGlyIleSerAlaGlyGlyTyrLysGlu 259
 QY 1671 TGTGAAGCTGACAACTCTGAGTGGGAAATTAATATGTAATATGATAGTAAATTTTAA 1730
 Db 260 CysProAsnAspArgMetCysGlyLysIleIleCysLysTyrGlnSerGluAsnIle 279
 QY 1731 TTCAAATTTCAAAGAGCCACTATTATTATCCCAACATAAGTGGACATCTCTGCTGCTCT 1790
 Db 280 LeuLysLeuArgSerAlaThrValIleTyrAlaAsnIleSerGlyIleValCysValSer 299
 QY 1791 GTGGAATTTGCCAGTATCATGACAGCAGCAAGATGGGATAAAGATGGAACCTCTCT 1850
 Db 300 LeuGluTyrProGlnGlyHisAsnGluSerGlnLysMetTrpValArgAspGlyThrVal 319
 QY 1851 TGTGGTTCAAATAAGGTTTTCAGGAATCAAAGATGTGTGAGTCTTCTCATCTCTGGGTAT 1910
 Db 320 CysGlySerAsnLysValCysGlnAsnGlnLysCysValAlaAspThrPheLeuGlyTyr 339
 QY 1911 GATTGTACTACTGACAAATGCAATGATAGAGGTGTATGCAATTAACAAAGACACTGTAC 1970
 Db 340 AspCysAsnLeuGluLysCysAsnHisGlyValCysAsnAsnLysLysAsnCysHis 359
 QY 1971 TGTAGTCTTCATATTACCTCCAGATGTCTCAGTCTCAATCAGATCTATGCGCTGGTGG 2030
 Db 360 CysAspProThrTyrLeuProProAspCysLysArgMetLysAspSerTyrProGlyGly 379
 QY 2031 AGTATTGACAGTGCATTTTCCACCTGTAGCTATATACCAGCAGACTCCCTGAAAGCGC 2090
 Db 380 SerIleAspSerGlyAsn--LysGluArgAlaGluPro-----IleProValArgPro 396
 QY 2091 TACATTGAGAACATTTTACCAATCCAAACCAATGAGATGGCCATTTTCTTATTCATCTCT 2150
 Db 397 TyrIleAlaSerArgTyrArgSerLysSerProArgTrpProPhePheLeuIlePro 416
 QY 2151 TTCTTTATTTTCTGTGTACTGATGCTATTAATGTTGAAGTTAATTTTCCAAAGGAAA 2210
 Db 417 PheTyrValValIleLeuValLeuIleGlyMetLeuValLysValTyrSerGlnArgMet 436
 QY 2211 AAATGGAACACTGAGGACTATTCAAGCGATGAGCAACCTCAAGATGAGAGTGAACCTAAA 2270
 Db 437 LysTrpArgMetAspPheSerSerGluGluGlnPheGluSerGluSerLys 456

RESULT 11

US-10-000-489-70
 ; Sequence 70, Application US/10000489
 ; Patent No. 6794363
 ; GENERAL INFORMATION:
 ; APPLICANT: Benjamin, Stephane
 ; APPLICANT: Tanaka, Hiroaki
 ; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 ; FILE REFERENCES: 91.US6.DIV
 ; CURRENT APPLICATION NUMBER: US/10/000,489
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: US 09/924,340


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Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
QY 1779 CTCTGCATCTCTGTGAATTTGCCAGTGAFCATGCAGACAGCCAAAGATGTGGATAAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
QY 1839 GATGGAACCTCTTGGTTCAAATAGTTTGCAGGATCAAGATGTGTGAGTTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
QY 1899 TACTTG-----GGTATGATTGACTACTACAAATGCAATGATGATAGAGGTGTATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
QY 1950 AATPAACAAAAGCACTGTCTACTGTAGTCTTCATATTTACTCCAGATTGCTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProProAsnCysGlnIleArg 656
QY 2010 TCAGATCTATGGCTGGTGGAGTATT-----CACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
QY 2058 GTAGTATACAGCCAGACTCCCTGAAGCGCTACATTGAGAACAATTTACCATTCCTCAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTCTCTTCTTTATTTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATTGCTATATGTTGAAGTTAATTTCCAAAGGAAATAATGGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysAsnTrpPheAlaLysGlu--- 714
QY 2232 TCAAGCGATGAGCAACTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 12
US-10-140-002-116
; Sequence 116, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 116
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-116
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Pred. No.: 2,27e-132 Length: 715
Score: 1493.50 Matches: 302
Percent Similarity: 56.67% Conservative: 123
Best Local Similarity: 40.27% Mismatches: 268
Query Match: 31.14% Indels: 57
DB: 4 Gaps: 14

US-10-054-683-18 (1-2640) x US-10-140-002-116 (1-715)

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Db 4 LeuLeuAlaLeuLeuThrGluLeuGlyArgLeuGlnAlaHisGluGlySerGluGlyLe 23
QY 138 CTGTGCAAAATTACAGTTCGGGAGAAAATAACGGTCAATAATAAAGGAAGAAATTTGAATCG 197
Db 24 PheLeuHisValThrValProArgLysIleLysSerAsnAspSerGluValSerGluArg 43
QY 198 CAGGCATCCTACAAAATTTGTAATTGAAGGAAACCATATATCTGTGAATTTAATGCAAAA 257
Db 44 LysMetIleTyrIleIleThrIleAspGlyGlnProTyrThrLeuHisLeuGlyLysGln 63
QY 258 AACTTTTACCCCAATAATTTTACAGTTTACAGTTTATAGTGGCACAGCAATTTATGAAACCA 317
Db 64 SerPheLeuProGlnAsnPheLeuValTyrThrTyrAsnGluThrGlySerLeuHisSer 83
QY 318 CTTGACCAAGATTTTCAGAAATTTCTGCCACTACCAAGGGTATATTTGAAGGTTATCCAAA 377
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Db 104 SerPheValThrLeuSerIleCysSerGlyLeuArgGlyPheLeuGlnPheGluAsnIle 123
QY 438 AGTTATGGATAGAACCCCTGGAGTCTTCAGTTGGCTTTCGACATGTAATTTTACCAAGTA 497
Db 124 SerTyrGlyIleGluProValGluSerSerAlaArgPheGluHisIleIleTyrGlnMet 143
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Db 144 LysAsnAsnAspProAsnValSerIleLeuAlaValAsnTyrSerHisIleTyrGlnLys 163
QY 552 GATCTGTCTTTAAATATCAAAAGCGGACGACAGCAAGATTTTGCAAG-----602
Db 164 AspGlnProTyrLysValProLeuAsnSerGlnIleLysAsnLeuSerLysLeuPro 183
QY 603 ---TATATAGAAATGCATGTTATAGTTGAAAACAATTTGTATATCATATGGGCTCTGAT 659
Db 184 GlnTyrLeuGluIleTyrIleIleValGluLysAlaLeu-----196
QY 660 ACAACTGTTGTCGCTCAAAAAGTTTCCAGTTGATTGAGTTCAGCAATGCTATTTTGT 719
Db 197 -----MetPheThr 199
QY 720 TCATTTAATATTAATAATTATCTGCTTCTTCAATGAGCTTTGGATAGATGAAATAAAT 779
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QY 780 GCAACCATCGGAGAACATAATGATGATTATACACACATTTTATAGATCGAAACATCTAT 839
Db 220 SerThrSerGlyAspAlaAspAspIleLeuGlnArgPheLeuAlaTrpLysArgAspTyr 239
QY 840 CTGTGTTTACGCTCTCATGATGGCATTTTACTTGTGTTTACAGAGAAAAGTCAAAATAT 899
Db 240 LeuIleLeuArgProHisAspIleAlaTyrLeuLeuValTyrArgLysHisProLysTyr 259
QY 900 GTTGTGTCACCTTTCAAGGGAAGATGTGTGTGTCACAACTATGCAGGAGGTGTGTCTG 959
Db 260 ValGlyAlaThrPheProGlyThrValCysAsnLysSerTyrAspAlaGlyIleAlaMet 279
QY 960 CACCCCGAAGCAATAGTCTGGAATCAGCTTGCAGTATTATTTAGTCAATTTAGGCTT 1019
Db 280 TyrProAspAlaIleGlyLeuGluGlyPheSerValIleIleAlaGlnLeuGlyLeu 299
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Db	210	LeuGluLeuValValValAenHisAspPhePheIleTyrSerGlnSerAsnIleSer	229
QY	666	GTGTGTCGCTCAAAAAGTTTTCCAGTTGATTGGAGTTGACGAATGCTATTTTGTGTTTCATTT	725
Db	230	LysValGlnGluAspValPheLeuValValAenIleValAsnIleValAspSerMetTyrGlnGlnLeu	249
QY	726	AATATTACAAATTATTCGTCTTCATTTGGAGCTTTGGATAGATGAAAATAAAATTTGCAACC	785
Db	250	GlyThrTyrrileleLeuIleGlyIleGluIleTyrAsnGlnGlyAenValPhePromet	269
QY	786	ACTGGAGAGCTAATGAGTTATTACACATTTTTTAAGATGGAAAAACATCTTATCTTGTGT	845
Db	270	Thr---SerIleGluGlnValLeuAenAspPheSerGlnTrrpLysGlnIleSerLeuSer	288
QY	846	TTACGTCCTCATGATGGCATTTTACTTGTGTTTACAGAGAAAAGTCAAATTTATGTTGGT	905
Db	289	GlnLeuGlnHisAspAlaHisMetPheIleLysAsnSerLeuIleSerIleLeuGly	308
QY	906	GCAACCTTTCAAGGGAAGATGTGTGATGCA-----AACTATGCA	944
Db	309	LeuAlaTyrValAlaGlyIleCysArgProProIleAspCysGlyValAspAenPheGln	328
QY	945	GGAGGTGTTGTTCTGCACCCCAAGACCATTAAGTCTGGAATCACTTGCAGTTATTTTAGCT	1004
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QY	1005	CAATTATTGAGCTTAGTATGGGATCACTTATGATGACATTAACAAATGCCAGTGCTCA	1064
Db	341	HisGluLeuGlyHisThrLeuGlyMetGlnHisAspGlu---GluPheCysPheCysGly	359
QY	1065	GGAGCTGTCTGCATTATGAATCCAGAAGCAATTCATTTTCAGTGGTGAAGATCTTTAGT	1124
Db	360	GluArgGlyCysIleMetAenThrPheArgVal-----ProAlaGluLysPheThr	376
QY	1125	AACTGCAGCTTCGAAGACTTTGCACATTTTATTTCAAAGCAGAAGTCCCAGTGTCTTCAC	1184
Db	377	AsnCysSerTyrAlaAspPheMetLysThrThrLeuAsnGlnGlySer---CysLeuHis	395
QY	1185	AATCAGCTCGCTTAGATCCTTTTTCAAACAGCAGCAGTGTGTGGTAAATGCAAGCTG	1244
Db	396	AsnProProArgLeuGlyGluIlePheMetLeuLysArg---CysGlyAenGlyValVal	414
QY	1245	GAAGCAGGAGAGAGTGTGACTGTGGAGCTGAACAGGATTTGTCCTTATTGGAGAAACA	1304
Db	415	GluArgGluGlnCysAspCysGlySerValGlnGlnCysGlu-----GlnAspAla	432
QY	1305	TGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAACCTGTGCTGAAGACCATTGC	1364
Db	433	CysCys---LeuLeuAenCysThrLeuArgProGlyAlaAlaCysAlaPheGlyLeuCys	451
QY	1365	TGGGAAAACGTCTATTATGTCAAAAGAAAGATGTGTAGGCCTTCCTTTGAAGAAATGC	1424
Db	452	CysLysAspCysLysPheMetProSerGlyGluLeuCysArgGlnGluValAenGluCys	471
QY	1425	GACCTCCCTGAAATTGCAATGGATCATCTGCATCATGCCAGAAAACCACTATGTTTCAG	1484
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QY	1485	ACTGGGCATCCGTGTGGAGCTGAATCAATGGATCTGTATAGATGGAGTTGTATGATGGGG	1544
Db	492	AspGlyIleProCysSerAspSerAlaTyr---CysTyrGlnLysArgCysAenAenHis	510
QY	1545	GATAAACAATGTACAGACACATTTGGCAAGAAGTAGAGTTTGGCCCTTCAGAAATGTTAT	1604
Db	511	AspGlnHisCysArgGluIlePheGlyLysAspAlaLysSerAlaSerGlnAenCysTyr	530
QY	1605	TCTCACCTTAATTCAAAGACTGATGTATCTGGAAACCTGTGGTATAGTATTAGTCAGGATAC	1664
Db	531	LysGluIleAenSerGlnGlyAenArgPheGlyHisCysGlyLysAenGlyThrThrTyr	550
QY	1665	ACACAGTGTGAAGCTGACAACTCTGCAGTCGGGAAAATTAATATGTAATATGTAGGTAAA	1724

Search completed: January 10, 2005, 22:09:27
Job time : 122 secs

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Db 397 AsnAlaPro---LeuProThrAspIleIleSerThrProIleCysGlyAsnGlnLeuVal 415
QY 1245 GAAGCAGGAGGAGGAGTGTGACTGTGGGACTCAACAGGAGTGTGCCCTTATTGGAGAAACA 1304
Db 416 GluMetGlyGluAspCysAspCysGlyThrSerGluGluCysThrAsnIle----- 432
QY 1305 TGCTGTGATATGCGCATGTAGATTTAAACCGGTTCAAACTGTGTGTAAGGACCAATGC 1364
Db 433 CysCysAspAlaIleThrCysIleIleLysAlaThrPheGlnCysAlaLeuGlyGluCys 452
QY 1365 TGGCAAACTGTCTATTATTGTCAAAAGAAGAATGTAGGCTTCCTTTGAAGATGC 1424
Db 453 CysGluLysCysGlnPheLysLysAlaGlyMetValCysArgProAlaLysAspGluCys 472
QY 1425 GACCTCCCTCAATATTGCAATGATCATCTGCATCGCCAGAAACCACTATGTTTCAG 1484
Db 473 AspLeuProGluMetCysAsnGlyLysSerGlyAsnCysProAspAspArgPheGlnVal 492
QY 1485 ACTGGGCATCCGTGTGGACTGAATCAATGATCTGTATAGATGAGGTTTGTATGAGTGGG 1544
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Db 513 GlnGluGlnCysThrGluLeuTrpGlyProGlyThrGluValAlaAspLysSerCysTyr 532
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Db 552 IleProCysLysAlaAsnAspThrMetCysGlyLysLeuPheCysGlnGlyGlySerAsp 571
QY 1713 -----TATGTAGTAATATTTTATCAAAATTCAGAGCCACTATTTATGTC 1763
Db 572 AsnLeuProTrpLysGlyArgIleValThrPheLeuThrCysLysThr----- 587
QY 1764 AACATAAGTGGACATCTCTGCATTGCTGTGGAATTTGCCAGTGTATGATGCAGACAGCAA 1823
Db 588 -----PheAspProGluAspThrSerGlnGlu 596
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QY 1884 TGCTGTG-----AGTTCTTTCATCTTGGTTTATCATTTGACTACTGACAAATGCAATGAT 1937
Db 617 CysValAspIleGluLysAlaIleLysSerThrAsnCysSerSer---LysCysLysGly 635
QY 1938 AGAGGTGTATGCAATAACAAAGCACTGTCTGCTAGTGTCTTCATATTTACCTCCAGAT 1997
Db 636 HisAlaValCysAspHisGluLeuGlnCysGlnCysGluGluGlyTrpIleProAsp 655
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Db 656 CysAspAspSerSer----- 660
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Db 661 -----ValValPheHisPheSer 666
QY 2118 CCAATGAGATGGCCATTTTCTTATTTCATCTCTTTTATTATTATTTCTGTGTACTGATT 2177
Db 667 IleValValGlyValLeuPhe-----ProMetAlaValIlePhe---ValValVal 682
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QY 2238 GATCAGCAACCTGAACT 2255
Db 698 AspGlnArgProLeuSer 703
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 10, 2005, 21:35:41 ; Search time 328.5 Seconds
(without alignments)
5795.484 Million cell updates/sec

Title: US-10-054-683-18

Perfect score: 4796

Sequence: 1 catctgcgacttcacactgc.....actgttacatttcacaaaaa 2640

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 3207808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications_AA -QFMT=fastn -SURFIX=n2p.rapb -MINMATCH=0.1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query
Result

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2	3984	83.1	734	14	US-10-205-823-10	Sequence 10, Appl
3	3984	83.1	734	17	US-10-473-603-19	Sequence 19, Appl
4	3969.5	82.8	735	14	US-10-205-823-8	Sequence 8, Appl
5	3900	81.3	753	14	US-10-205-823-6	Sequence 6, Appl
6	1530	31.9	820	10	US-09-961-656-2	Sequence 2, Appl
7	1524.5	31.8	787	14	US-10-227-884-90	Sequence 90, Appl
8	1524.5	31.8	787	14	US-10-230-163-90	Sequence 90, Appl
9	1524.5	31.8	787	14	US-10-230-338-90	Sequence 90, Appl
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28	1524.5	31.8	787	14	US-10-216-165-90	Sequence 90, Appl
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ALIGNMENTS

RESULT 1

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; Sequence 19, Application US/10054683
; Publication No. US20030044813A1
; GENERAL INFORMATION:
; APPLICANT: Old, Lloyd J.
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Chen Yao-Tseng
; TITLE OF INVENTION: Cancer-Testis Antigens
; FILE REFERENCE: L0461/7125 (JRV)
; CURRENT APPLICATION NUMBER: US/10/054, 683
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/280, 718
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/285, 154
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/327, 432
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 734

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-054-683-19

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Percent Similarity: 100.00% Conservative: 0
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721 SerSerAspGluGlnProGluSerGluSerGluProLysGly 734

RESULT 2

US-10-205-823-10
; Sequence 10, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsay, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-10

Alignment Scores:
Pred. No.: 0 Length: 734
Score: 3984.00 Matches: 734
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.07% Indels: 0
DB: 14 Gaps: 0

US-10-054-683-18 (1-2640) x US-10-205-823-10 (1-734)

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1 MetTrpValLeuPheLeuSerGlyLeuGlyLeuArgMetAspSerAsnPheAsp 20
QY 132 AGTTACCTGTGCAATACAGTCCGGAGAAATACGGTCAATATAAAGAGGAAATT 191
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21 SerLeuProValGlnIleThrValProGluLysIleArgSerIleIleLysGluGly 40

QY 192 GAATCCAGGCATCTCTACAAAAATTGTAATTGAAGGAAACCATATATCTGTGAATTTAATG 251
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41 GluSerGlnAlaSerTyrLysIleValIleGluGlyLysProTyrThrValAsnLeuMet 60
QY 252 CAAAAAATCTTTTACCCCATATTTTACAGTTTACAGTTTATAGTGGCAGCAAGTAATG 311
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61 GlnLysAsnPheLeuProHisAsnPheArgValTyrSerTyrSerGlyThrGlyIleMet 80
QY 312 AAACCACTTGACCAAGATTTTCAGAAATTTCTGCCACTTACCAAGGGTATATTGAAGGTTAT 371
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81 LysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGlyTyr 100
QY 372 CCAAAATCTGTGTGTGATGTTAGCATGTACTGAGCTCAGGGCGGTACTACAGTTTGAA 431
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101 ProLysSerValValMetValSerThrCysThrGlyLeuArgGlyValLeuGlnPheGlu 120
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121 AsnValSerTyrGlyIleGluProLeuGluSerValGlyPheGluHisValIleTyr 140
QY 492 CAAATAAACATAAGAAAGCAGATGTTTCTTATATAATGAGAAGATATTGAATCAAGA 551
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141 GlnValLysHisLysLysAlaAspValSerLeuTyrAsnGlnLysAspIleGluSerArg 160
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341 AlaIleHisPheSerGlyValLysIlePheSerAsnCysSerPheGluAspPheAlaHis 360
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QY 1452 TCTGCATCATGCCAGAAAACCATATGTTTCAGACTGGGCATCGGTGGGACTGAATCAA 1511
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US-10-473-603-19
; Sequence 19, Application US/10473603
; Publication No. US20040235066A1
; GENERAL INFORMATION:
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; APPLICANT: OLD, Lloyd
; APPLICANT: SCANLAN, Matthew
; APPLICANT: CHEN, Yao-Tseng
; TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
; FILE REFERENCE: 10461.70155US00
; CURRENT APPLICATION NUMBER: US/10/473.603
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/US02/09808
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 10/054.683
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/280.718
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/285.154
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/327.432
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-473-603-19
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Alignment Scores:
Pred. No.: 0 Length: 734
Score: 3984.00 Matches: 734
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.07% Indels: 0
DB: 17 Gaps: 0
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US-10-054-683-18 (1-2640) x US-10-473-603-19 (1-734)

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Db 41 GluSerGlnAlaSerTyrLysIleValIleGluGlyLysProTyrThrValAsnLeuMet 60
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QY 312 AAACCACTTGACCAAGATTTTCAGATTTTCTGCCACTACCAAGGTATATTGAAGTTAT 371
Db 81 LysProLeuAspGlnAspPheGlnAsnPheCysHisTyrGlnGlyTyrIleGluGlyTyr 100
QY 372 CAAAAATCTGTGTGATGTTAGTACCATGTCTGAGCTCAGGGGCTGCTACTACAGTTTGA 431
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QY 492 CAAGTAAAAACATAAGAAACAGATTTTCTCTATATAATGAGAAGGATATTGAAATCAAGA 551
Db 141 GlnValLysHisLysLysAlaAspValSerLeuTyrAsnGluLysAspIleGluSerArg 160
QY 552 GATCTCTCTCTTTAAATTAACAAAGCGCAGAGCCAGCAAGATTTTGCAAAGTATATAGAA 611
Db 161 AspLeuSerPheLysLeuGlnSerAlaGluProGlnGlnAspPheAlaLysTyrIleGlu 180
QY 612 ATGCATGTTATAGTTGAAAAACAATTTGATATCATATGCTGGGTCTGATCAACTGTTGTC 671
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Qy 1512 TGGATCTGTATAGATGGAGTTTCTGATGAGTGGGATAAACAATGTCACAGACATTTGGC 1571
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Qy 1572 AAAGAAGTAGAGTTTGGCCCTTCAGAAATGTTATTCTCACCTTAATTCAAAAGACTGTGTA 1631
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Qy 1872 AGAAATCAAGATGTGTGAGTCTTTCATACTTCGGTTTATGATTGTACTACTGACAAATGC 1931
Db 601 ArgAsnGlnArgCysValSerSerSerTyrLeuGlyTyrAspCysThrThrAspLysCys 620
Qy 1932 AATGATAGAGGTGTGATGCAATAACAAAAGCAGTGCACCTGTAGTGTCTTATTTACCT 1991
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RESULT 4

US-10-205-823-8
; Sequence 8, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 735

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-8

Alignment Scores:
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Score: 3969.50 Matches: 733
Percent Similarity: 99.73% Conservative: 0
Best Local Similarity: 99.73% Mismatches: 1
Query Match: 82.77% Indels: 1
DB: 14 Gaps: 1

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QY 1149 CATTTTATTTCAAGCAGAAAGTCCAGTGTCTTCACAATCAGCTCGCTTAGTATCCTTTT 1208
DB 361 HisPheIleSerLysGlnLysSerGlnCysLeuHisAsnGlnProArgLeuAspPhe 380
QY 1209 TTCAACAGCAAGCAGTGTGTGTAATTCGAAAGCTGGAAGCAGAGAGGAGTGTGACTGT 1268
DB 381 PheLysGlnGlnAlaValCysGlyAsnAlaLysLeuGluAlaGlyGluCysAspCys 400
QY 1269 GGGACTGAACAGGATTTGTGCCCTTATTTGGAGAAACATGCTGTGTATATATGACATGTAGA 1328
DB 401 GlyThrGluGlnAspCysAlaLeuIleGlyGluThrCysCysAspIleAlaThrCysArg 420
QY 1329 TTTAAAGCCGTTTCAAACTGTGCTGAAGGACCATGCTGCCAAAACATGCTCTATTATGTCA 1388
DB 421 PheLysAlaGlySerAsnCysAlaGluGlyProCysCysGluAsnCysLeuPheMetSer 440
QY 1389 AAAGAAGAAATGTGTAGGCTTCTCTTTGAAGAATGCGACCTCCCTGTAATATTCGAATGGA 1448
DB 441 LysGluArgMetCysArgProSerPheGluGluCysAspLeuProGluTyrCysAsnGly 460
QY 1449 TCATCTGCATCATGCCAGAAAACCATGTTTTCAGACTGGGCTCGCTGTGACTGCAAT 1508
DB 461 SerSerAlaSerCysProGluAsnHisTyrValGlnThrGlyHisProCysGlyLeuAsn 480
QY 1509 CAATGGATCTGTATAGATGAGTTTGTATGAGTGGGATATAACAATGTACAGACACATTT 1568
DB 481 GlnTrpIleCysIleAspGlyValCysMetSerGlyAspLysGlnCysThrAspThrPhe 500
QY 1569 GGCAAGAGATAGAGTTTGGCCCTTCAGAAATGTTATTTCTCACCTTAAATTCAAAGACTGAT 1628
DB 501 GlyLysGluValGluPheGlyProSerGluCysTyrSerHisLeuAsnSerLysThrAsp 520
QY 1629 GTATCTGGAACTGTGTTAAGTAACTGATTCAGGATACACAGTGTGAAGCTGACATCTG 1688
DB 521 ValSerGlyAsnCysGlyIleSerAspSerGlyTyrThrGlnCysGluAlaAspAsnLeu 540
QY 1689 CAGTGGCGAAAAATTAATATGTAATAATATGATAGTAAATTTTATTACAAATTCCAAGAGCC 1748
DB 541 GlnCysGlyLysLeuIleCysLysTyrValGlyLysPheLeuLeuGlnIleProArgAla 560
QY 1749 ACTATTATTTATGCCAACATAAGTGGACATCTCTGCAATGCTGTGGAATTTGCCAGTAT 1808
DB 561 ThrIleIleTyrAlaAsnIleSerGlyHisLeuCysIleAlaValGluPheAlaSerAsp 580
QY 1809 CATGCAGACAGCCAAAGATGTGGATAAAGATGGAACCTTCTGTGTTCAAAATAGGTT 1868
DB 581 HisAlaAspSerGlnLysMetTrpIleLysAspGlyThrSerCysGlySerAsnLysVal 600
QY 1869 TGCAAGAATCAAAAGATGTGTGAGTCTTCTCATCTTGGGTTTATGATTGTACTACTGACAAA 1928
DB 601 CysArgAsnGlnArgCysValSerSerTyrLeuGlyTyrAspCysThrThrAspLys 620
QY 1929 TGAATGATAGAGGTGTATGCAATAACAAAGACATGTCTGCTAGTGTGCTTCAATTTA 1988
DB 621 CysAsnAspArgGlyValCysAsnAsnLysLysHisCysHisCysSerAlaSerTyrLeu 640
QY 1989 CTTCCAGATTGCTCAGTTCATTCAGATCTATGCTGCTGGAGTATTCACAGTGCACAT 2048
DB 641 ProProAspCysSerValGlnSerAspLeuTrpProGlyLysIleAspSerGlyAsn 660
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Qy 1245 GAAGCAGGAGGAGTGACTGTGGGACTGACACAGGATGTGCCCTTATTGGAGAAACA 1304
Db 411 GluAlaGlyGluGluCysAspCysGlyThrGluGlnAspCysAlaLeuIleGlyGluThr 430
Qy 1305 TGCTGTGATATGCCACATGTAGATTTAAAGCCGGTTCAAAGTGTGCTGAGAGGACCATGC 1364
Db 431 CysCysAspIleAlaThrCysArgPheLysAlaGlySerAsnCysAlaGluGlyProCys 450
Qy 1365 TGGCAAACTCTCTATTATGTGCAAAAGAAAGATGTGTAGCCCTCTCTTTGAAGATGC 1424
Db 451 CysGluAsnCysLeuPheMetSerLysGluArgMetCysArgProSerPheGluGluCys 470
Qy 1425 GACCTCCCTGAATATTGCAATGGATCATCTGCATCATGCCAGAAAACCATATGTTTCAG 1484
Db 471 AspLeuProGluTyrCysAsnGlySerSerAlaSerCysProGluAsnHisTyrValGln 490
Qy 1485 ACTGGGCATCCGTGGACTGAATCAATGGATCTGTATAGATGGAGTTGTGATGAGTGGG 1544
Db 491 ThrGlyHisProCysGlyLeuAsnGlnTrpIleCysIleAspGlyValCysMetSerGly 510
Qy 1545 GATAAACAATGTACAGACACATTTGGCAAGAGATGTGTAGGTTTGGCCCTTCAGAAATGTTAT 1604
Db 511 AsplysGlnCysThrAspThrPheGlyLysGluValGluPheGlyProSerGluCysTyr 530
Qy 1605 TCTCACCTTAATCAAGACTGATGTATCTGAAACTGTGTATAAGTGTATCAGGATAC 1664
Db 531 SerHisLeuAsnSerLysThrAspValSerGlyAsnCysGlyIleSerAspSerGlyTyr 550
Qy 1665 ACACAGTGTGAGCTGACAACTCGCAGTCCGGAATAATATGTAATATGTTAGTTAAA 1724
Db 551 ThrGlnCysGluAlaAspAsnLeuGlnCysGlyLysLeuIleCysLysTyrValGlyLys 570
Qy 1725 TTTTATTACAAATTCGAAGCACTATTATTATGTCACATCAATAGTGGACATCTCTGC 1784
Db 571 PheLeuLeuGlnIleProArgAlaThrIleIleTyrAlaAsnIleSerGlyHisLeuCys 590
Qy 1785 ATTGCTGTGGAATTTGCCAGTGTATGACAGACCCAAAGATGTGTGATAAAGATGGA 1844
Db 591 IleAlaValGluPheAlaSerAspHisAlaAspSerGlnLysMetTrpIleLysAspGly 610
Qy 1845 ACTTCTGTGCTTCAAAATAGGTTGACAGGATCAAGATGTGTGAGTCTTCTACTATTG 1904
Db 611 ThrSerCysGlySerAsnLysValCysArgAsnGlnArgCysValSerSerTyrLeu 630
Qy 1905 GGTATGATTGTACTACTGACAAATGCAATGATAGAGTGTATGCAATAACAAAAGCAC 1964
Db 631 GlyTyrAspCysThrThrAspLysCysAsnAspArgGlyValCysAsnAsnLysLysHis 650
Qy 1965 TGTCACTGTAGTCTTCAATATTATCTCCAGATTGCTCAGTTCAATCAGATCTATGGCCT 2024
Db 651 CysHisCysSerAlaSerTyrLeuProProAspCysSerValGlnSerAspLeuTrpPro 670
Qy 2025 GGTGGAGATTGACAGTGGCAATTTCCACTGTAGCTATACAGCCAGACTCCCTGAA 2084
Db 671 GlyGlySerIleAspSerGlyAsnPheProProValAlaIleProAlaArgLeuProGlu 690
Qy 2085 AGGCGCTACATTGAGAACATTTACCATTCCAAACCAATGAGATGCCATTTTCTTATTC 2144
Db 691 ArgArgTyrIleGluAsnIleTyrHisSerLysProMetArgTrpProPhePheLeuPhe 710
Qy 2145 ATTCTCTTCTTATTATTTCTGTACTGATGCTATATGTTGGTGAAGTAAATTTCCAA 2204
Db 711 IleProPhePheIleIlePheCysValLeuIleAlaIleMetValLysValAsnPheGln 730
Qy 2205 AGGAAAAATGGAGAACTGAGGACTATTCAAGCCATGAGCAACTGAAAGTGACAGTGAA 2264
Db 731 ArgLysLysTrpArgThrGluAspTyrSerSerAspGluGlnProGluSerGluSerGlu 750
Qy 2265 CCTAAAGG 2273
Db 751 ProLysGly 753

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RESULT 6

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US-09-961-656-2
; Sequence 2, Application US/09961656
; Publication No. US20030017572A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 56294, 56629, NOVEL HUMAN
; FILE REFERENCE: 10448-092002
; CURRENT APPLICATION NUMBER: US/09/961,656
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/235,035
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-656-2

Alignment Scores:
Pred. No.: 1,27e-126 Length: 820
Score: 1530.00 Matches: 318
Percent Similarity: 57.84% Conservative: 132
Best Local Similarity: 40.87% Mismatches: 266
Query Match: 31.90% Indels: 62
DB: 10 Gaps: 20

US-10-054-683-18 (1-2640) x US-09-961-656-2 (1-820)
Qy 6 CGCATTCCAACTCCCTGTACCAACCACTGCCCTTATTCGGCTCGGACCCAGGACTT 65
Db 22 ArgThrArgGlyCys-----TTPGlnProArgSer 31
Qy 66 CAAGCCATGTGGTCTTGTMTT---CTGCTCAGCGGGCTCGCGGGCTCGCGATGGAC--- 119
Db 32 ArgThrMetPheArgLeuTrpLeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArg 51
Qy 120 AGTAATTTTGATGTTTACCTGTGCAATTTACAGTTCCGAGAAATACCGTCAATAATA 179
Db 52 ProGlyPheGlnAsnSerLeuLeuGlnIleValIleProGluLysIleGlnThrAsnThr 71
Qy 180 AAGCAAGCAATTCGA-----TCGCGAGCATCTTACAAAATTTGTAATTAAGGAGAA 230
Db 72 AsnAspSerSerGluIleGluTyrGluGlnIleSerTyrIleIleProIleAspGluLys 91
Qy 231 CCATATCTGTGAATTTAATGCAAAAACCTTTTACCCCATATTTTAGAGTTTACAGT 290
Db 92 LeuTyrThrValHisLeuLysGlnArgTyrPheLeuAlaAspAsnPheMetIleTyrLeu 111
Qy 291 TATAGTGGCAGCAAGATTATGAACCACTTGACCAAGATTTTTCAGATTTTCCCATAC 350
Db 112 TyrAsn---GlnGlySerMetAsnThrTyrSerSerAspIleGlnThrGlnCysTyrTyr 130
Qy 351 CAAGGGTATATTCAAGGTATTCAAAATCTGTGGTGTATGCTAGCATCTACTTGGACTC 410
Db 131 GlnGlyAsnIleGluGlyTyrProAspSerMetValThrLeuSerThrCysSerGlyLeu 150
Qy 411 AGGGCGCTACTACAGTTTGAATGTTAGTTATGGAATAGAACCCCTCGGAGTCTTCAATT 470
Db 151 ArgGlyIleLeuGlnPheGluAsnValSerTyrGlyIleGluProLeuGluSerAlaVal 170
Qy 471 GGCTTTGAACATCTAATTTACCAAGTAATAACATAAGAACAGATGTTTCTCTATATAAT 530
Db 171 GluPheGlnHisValLeuTyrLysLeuLysAsnGluAsnAspIleAlaIlePheIle 190
Qy 531 GAGAAGGATATTGAATCAACA-----GATCTGTCTCTTAAATTTACAAAGCGCAGAG 581
Db 191 AspArgSerLeuLysGluGlnProMetAspAsnIlePheIleSerGluLysSerGlu 210
Qy 582 CCACAGCAAGAT-----TTTGCAAGATATATAGAAATGCATGTTATAGTTGAAAAACA 635

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Db 538 LysTyrValPheCysGlyTyrArgAsnLeuLeuCysGlyArgLeuValCysThrTyrPro 557
Qy 1719 GGTAAATTTTATACAAATCCAAAGCCACTATTATATGCAACATAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
Qy 1779 CTCTGCAATTCGTGGAAATTTGCCAGTGATCATGCAGACAGCCAAAAGATGTGGATAAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
Qy 1839 GATGGAATCTTGTGGTGCATTAAGTTGTCAGGAATCAAGATGTGTGAGTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
Qy 1899 TACTTG-----GCTTATGATTGCTACTGACAAATGCAATGATAGAGGTGATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
Qy 1950 AATAACAAAAGCACTGCTACTGTAGTGCTTTCATATTATTCCTCAGATTCGTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProProAsnCysGlnIleArg 656
Qy 2010 TCAGATCTATGCTGCTGGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
Qy 2058 GTAGCTATACAGCCAGCACTCCCTGAAAGCGCTACATTCGAAACATTTACCATCCAAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
Qy 2118 CCAATGAGATGG-----CCATTTTCTTATTCATCTCTTTTATTATTTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
Qy 2172 CTGATCTCTAATGTGGAAGTTAATTTCAAGGAAAATGGAAGTGGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLysLysTrpPheAlaLysGlu--- 714
Qy 2232 TCAAGCATGAGCAACTGAAAGTGAGAGTGAACCTAAAGG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 8
US-10-230-163-90
; Sequence 90, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627

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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
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; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
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; PRIOR APPLICATION NUMBER: 60/141037
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; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
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; PRIOR APPLICATION NUMBER: 60/146222
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; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
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; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Alignment Scores:
Pred. No.: 3,87e-126 Length: 787
Score: 1524.50 Matches: 310
Percent Similarity: 58.89% Conservative: 134
Best Local Similarity: 41.11% Mismatches: 259
Query Match: 31.79% Indels: 51
DB: 14 Gaps: 18

US-10-054-683-18 (1-2640) x US-10-230-163-90 (1-787)
QY 72 ATGTGGTCTTGTTCCTCAGCGGGCTCGGGGGCTGGGATGGAC---AGTAATTTT 128
Db :::: LeuTriLeu-----LeuLeuAlaGlyLeuCyAsGlyLeuLeuAlaSerArgProGlyPhe 21
QY 129 GATAGTTTACCTGCGAAATTACAGTTCGGAGAAATACGGTCAATAATAAAGGAAGGA 188
Db :::: GlnAsnSerLeuLeuGlnIleValIleProGluLysIleGlnThrAsnThrAsnAspSer 41
QY 189 ATTGAA-----TCGCAGGCATCTACAAAATTGTAATTCAAGGGAACCATATACT 239
Db :::: SerGluIleGluTyrrGluGlnIleSerTyrrIleIleProIleAspGluLysLeuTyrrThr 61
QY 240 GTGAATTTAATGCAAAAAAATTTTATCCCATATAATTTTAGAGTTTACAGTTTACAGTTAGTGC 299
Db :::: ValHisLeuLysGlnArgTyrrPheLeuAlaAspAsnPheMetIleTyrrLeuTyrrAsn--- 80
QY 300 ACAGGAATTATGAAACCACTTGACCAAGATTTTCAGAAATTTCTGCCACTACCAAGGATAT 359
Db :::: GlnGlySerMetAsnThrTyrrSerSerAspIleGlnThrGlnCysTyrrTyrrGlnGlyAsn 100
QY 360 ATTGAAGGTTATCCAAAATCTGGTGGTGGTGTAGCACATGTACTGTGACTCAGGGCGGTA 419
Db :::: IleGluGlyTyrrProAspSerMetValThrLeuSerThrCysSerGlyLeuAsGlyIle 120
QY 420 CTACAGTTTGAATAATCTTAGTTATGAATAGAACCCCTCGAGTCTTCAGTTGGCTTTGAA 479
Db :::: LeuGlnPheGluAsnValSerTyrrGlyIleGluProLeuGluSerAlaValGluPheGln 140
QY 480 CATGTAATTTACCAAGTAAACATAGAAGACAGATGTTTCCTTATATATATAGNAGGAT 539
Db :::: HisValLeuTyrrLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer 160
QY 540 ATTGAATCAAGA-----GATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 590
Db :::: LeuLysGluGlnProMetAspAspAsnIlePheIleSerGluLysSerGluProAlaVal 180
QY 591 GAT-----TTTCAAAGTATATAGAAATGTCATGTTATAGTTGAAAAACAATTGTATAAT 644
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Db 181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspLysThrLeuTyrAsp 200
Qy 645 CATATGGGCTGTGATACAACTGTGTGCTCAAAAAGTTTCCAGTTGATGGATTGACG 704
Db 201 TyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluIleValGlyLeuAla 220
Qy 705 AATGCTATTTTGTTCATTTAATTAACAATTATCTGTCTTCATTTGGAGCTTTGGATA 764
Db 221 AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGluLeuTyrSer 240
Qy 765 GATGAAATAAATGCAACCACTGGAGAACTAATAGATTATTAACACATTTTAAAGA 824
Db 241 AspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuLeuGlnLysPheLeuGlu 260
Qy 825 TGGAAACATCTTATCTGTGTTCAGTCTCATGATGGCATTTTACTTGTGTACAGA 884
Db 261 TrpLysGlnSerTyrLeuAsnLysArgProHisAspIleAlaTyrLeuLeuIleTyrMet 280
Qy 885 GAAAGTCAAAATATGTTGGTCAACCTTTCAAGGGAAGATGTGTGATGCAAACTATGCA 944
Db 281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
Qy 945 GGAGGTGTTTGTGACCCCAAGCAACCAATAGTCTGGAATCACTTGGAGTTATTTAGCT 1004
Db 301 AlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
Qy 1005 CAATTATTGAGCTTAGTATGGGATCACTTATGATGACATTAACAATGCCAGTGTCA 1064
Db 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCysGlnCysSer 340
Qy 1065 GGAGCTGTGCTGATTAATGCAAGCAATTCATTTAGTGTGTGAAGATCTTTAGT 1124
Db 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
Qy 1125 AACTGAGCTTCGAAGACTGTGCACATTTATTTTCAAGCAAGATCCAGTGTCTTAC 1184
Db 361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
Qy 1185 AATCAGCTCGCTAGATCCTTTTCAACAGCAAGCAGTGTGTGTAATGCAAGCTG 1244
Db 381 AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
Qy 1245 GAAGCAGGAGGAGTGTGATGTGGGACTGAACAGGATTTGTCCTTTATTTGGAGAACA 1304
Db 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
Qy 1305 TGCTGTGATATGGCAATGATAGATTTAAACCGGTTCAACTGTGTGAGGACCATGC 1364
Db 418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
Qy 1365 TGCAGAACTGTCTATTATTATCAAAAGAAAGATGTAGGCT---TCCTTTGAAGAA 1421
Db 438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
Qy 1422 TGCAGCTCCCTGAATATTGCAATGGATCATCTGCATCATGCCAGAAACCACTATGTT 1481
Db 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
Qy 1482 CAGACTGGCATCCGTGTGACTGAATCAATGATGATCTGTATAGATGGAGTTTGTAGT 1541
Db 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGlyAspCysHisAsp 497
Qy 1542 GGGATAAACAATGTACAGACACATTTGGCAAGAAAGTAGATTTGGCCCTTCAGATGT 1601
Db 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
Qy 1602 TATTCTCACCTTAATCAAGACTGATGTATCTCGAACTGTGTGATAAGT---GATTCA 1658
Db 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
Qy 1659 GGATACACAGTGTGAAGCTGACAATCTGCAGTGGCGGAAATTAATATGTAATATGTA 1718

Db 538 LysTyrValPheCysGlyTyrArgAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
Qy 1719 GGTAAATTTTATTACAAATTTCCAGAGCCACTATTATTATTCACACATAAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
Qy 1779 CTCTGATCTCTCTGGAATTTGCGAGTGATCATCGACAGCCCAAGAGATGTGGATAAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
Qy 1839 GATGGAACCTTCTTGTGTTCAATAAGTTTGCAGGAATCAAAAGATGTGTGAGTTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValAsnArgGluCysValGluSerArg 617
Qy 1899 TACTTG-----GGTTATGATTGTACTACTACGAAATGCAATGATAGAGTGTATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
Qy 1950 AATAACAAAGCACTGTCTACTGTAGTCTTCATATTACTCCAGATTGCTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProAsnCysGlnIleArg 656
Qy 2010 TCAGATCTATGGCTGTGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
Qy 2058 GTAGCTATACAGCCAGACTCCTCTGAAAGCGCTACATTGAGAACATTTACCATTCCAAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
Qy 2118 CCAATGAGATGG-----CCATTTTCTTATTATTCCTTCTTTATTATTATTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
Qy 2172 CTGATTGCTATAATGTGTGAAGTTAATTTCCAAAGGAAAAAATGAGAACTGAGGACTAT 2231
Db 697 ---ThrThralaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
Qy 2232 TCAAGCGATGAGCAACTGAAAGTGAGAGTGAACTAAAGGG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 9

US-10-230-338-90
; Sequence 90, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P35301C92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31

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; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 90
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-90

Alignment Scores:
Pred. No.: 3,87e-126 Length: 787
Score: 1524.50 Matches: 310
Percent Similarity: 58.89% Conservative: 134
Best Local Similarity: 41.11% Mismatches: 259
Query Match: 31.79% Indels: 51
DB: 14 Gaps: 18

US-10-054-683-18 (1-2640) x US-10-230-338-90 (1-787)

QY 72 ATGTGGTCTGTTCTCTCAGCGGCTCGGGGGCTGGGATGGAC---AGTAATTTT 128
DB 4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21
QY 129 GATAGTTTACCTGTGCAAAATTCAGCTTCCGGAGAAATACGGTCAATAATAAAGGAAGGA 188
DB 22 GluAsnSerLeuLeuGlnIleValIleProGluIleGlnThrAsnThrAsnAspSer 41
QY 189 ATTGAA-----TCGAGGCAATCCTACAAATTTGTAATTTGAAGGGAACCATATACT 239
DB 42 SerGluIleGluTyrGluGlnIleSerTyrIleIleProIleAspGluIysLeuTyrThr 61
QY 240 GTGAATTTAATGCAAAAACCTTTTACCCCAATAATTTTAGAGTTTACAGTTTACAGTGGC 299
DB 62 ValHisLeuIysGlnArgTyrPheLeuAlaAspAsnPheMetIleTyrLeuTyrAsn--- 80
QY 300 ACAGGAATATGAAACCACTTGACCAAGATTTTCAGAAATTTTCCCACTACCAAGGGTAT 359
DB 81 GluGlySerMetAsnThrTyrSerSerAspIleGlnThrGlnCysTyrTyrGlnGlyAsn 100
QY 360 ATTGAAGTTATCAAAATCTGTGGTATGGTAGCAGCATGTACTGGAGCTCAGGGCGTA 419
DB 101 IleGluGlyTyrProAspSerMetValThrLeuSerThrCysSerGlyLeuArgGlyIle 120
QY 420 CTACAGTTTCAAAATGTTAGTATGGAATAGAACCCCTGAGTCTTCAGTTGGCTTTGAA 479
DB 121 LeuGlnPheGluAsnValSerTyrGlyIleGluProLeuGluSerAlaValGluPheGln 140
QY 480 CATGTAATTTACCAAGTAAACATAAGAAAGCAGATGTTTCCTTATATATAGAGAGAT 539
DB 141 HisValLeuTyrIysLeuIysAsnGluAspAsnAspIleAlaPheIleAspArgSer 160
QY 540 ATTGAATCAAGA-----GATCTGCTCTTTAAATTAACAAGCGCAGACCCACAGCAA 590
DB 161 LeuIysGluGlnProMetAspAspAsnIlePheIleSerGluIysSerGluProAlaVal 180
QY 591 GAT-----TTTGCAGATATAGAAATCATCTATATAGTTGAAACAAATTTGATAAT 644
DB 181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspIysThrLeuTyrAsp 200
QY 645 CATATGGGCTCTGATACAACTGTGTGCTCGCTCAAAAAGTTTTTCCAGTTGATTGGATGACG 704
DB 201 TyrTrpGlySerAspSerMetIleValThrAsnIysValIleGluIleValGlyLeuAla 220
QY 705 AATGCTATTTTGTCTTCAATTAATTAATTAATTAATTTCTGCTCTTCTGGAGCTTTGGATA 764
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DB 221 AsnSerMetPheThrGlnPheIysValThrIleValLeuSerSerLeuGluLeuTrpSer 240
QY 765 GATGAAATAAATAATTCACCACTGGAGAAAGCTAATCAGTTATTACACACATTTTTAAGA 824
DB 241 AspGluAsnIysIleSerThrValGlyGluAlaAspGluLeuLeuGlnIysPheLeuGlu 260
QY 825 TGGAAACATCTTATCTTGTGTCTCTCATGATGTGGCATTTTACTGTTTACAGA 884
DB 261 TrpIysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaTyrLeuLeuIleTyrMet 280
QY 885 GAAAAGTCAAATATATGTTGTGCAACCTTTTCAAGGGAAGATGTGTATGCAAACTATGCA 944
DB 281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
QY 945 GGAGGTGTTTCTGCACCCACCAACCAATAGTCTCGAATCACTTGCAGTTATTTAGCT 1004
DB 301 AlaGlyValAlaLeuTyrProIysGluIleThrLeuGluAlaPheAlaValIleValThr 320
QY 1005 CAATATTAGCCTTAGTAGTGGGATCACTTATGATGACATTAAACAAATCCAGTGTCTCA 1064
DB 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProIysIysCysGlnCysSer 340
QY 1065 GGAGCTGCTGCTATTAATCCAGAGCAATTCATTTCAGTGGTGTGAAGATCTTTAGT 1124
DB 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValIysThrPheSer 360
QY 1125 AACTGAGCTTCGAAGACTTTGCACATTTTATTTTCAAGCAGAAAGTCCCAAGTCTTTCAC 1184
DB 361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValIysCysLeuGln 380
QY 1185 AATCAGCCTCGCTTAGATCCTTTTTCAAACACAGACAGATGTGTGTATGCAAGCTG 1244
DB 381 AsnIysProGlnMetGlnIys---LysSerProIysProValCysGlyAsnGlyArgLeu 399
QY 1245 GAAGCAGGAGAGAGTGTGACTGTGGAGCTGAACAGATGTGTCCCTTATTTGGAGAAACA 1304
DB 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
QY 1305 TGCTGTGATATTGCCCATGTAGATTTAAAGCCGTTTCAAACTGTGCTGAAGGACCATGC 1364
DB 418 CysCysAspPheArgThrCysValLeuIysAspGlyAlaIysCysTyrIysGlyLeuCys 437
QY 1365 TCGAAAACCTGCTATTATTTATGTCAAAGAAAGAAATGTGTAGCGCT---TCCTTTGAAGAA 1421
DB 438 CysIysAspCysGlnIleLeuGlnSerGlyValGluCysArgProIysAlaHisProGlu 457
QY 1422 TCGCAGCTCCTCAATATTGCAATGATCATCTGCATCATCTGCCAGAAACCATATGTT 1481
DB 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
QY 1482 CAGACTGGGCATCCGTGTGAGCTGAATCAATGATCTGTATAGATGGAGTTTGTATCAGT 1541
DB 478 IleAsnGlyLeuSerCysIysAsnAsnIysPheIleCysTyrAspGlyAspCysHisAsp 497
QY 1542 GGGGATAAACAATGTACAGACACATTTGGCAAGAAGTAGTAGTTTGGCCCTTCAGAAATGT 1601
DB 498 LeuAspAlaArgCysGluSerValPheGlyIysGlySerArgAsnAlaProPheAlaCys 517
QY 1602 TATTCACCTTAATTAAGAAGCTGATGATCTGGAAACTGTGTGTATAGT---GATTCA 1658
DB 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
QY 1659 GGATACACAGTGTGAAGCTGACAATCTGACGTGCGGAAAATTAATATCTATAATGTA 1718
DB 538 LysTyrValPheCysGlyTrpArgAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
QY 1719 GGTAATTTTATTACAAATTTCCAAGACCATCTATTATTATGCCAACATAAGTGGACAT 1778
DB 558 ThrArgIysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
QY 1779 CTCTGATCTGCTGGAAATTTGCCAGTGCATCATGCAGACAGCCAAAGATGTGTGATAAAA 1838
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578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597

1839 GATGGAACTCTCTTGCTTCAAAATAAGGTTTCAGAGGAATCAAGATGCTGAGTTCTTCA 1898

598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617

1899 TACTWG-----GGTTATGATGTACTACTGACAAATGCAATGCAATGATAGAGGTGTATGC 1949

618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636

1950 AATAACAAAAGCACTGCTACTGTAGTGCCTTCATATTTACCTCAGATTGCTCAGTTCAA 2009

637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProAsnCysGlnIleArg 656

2010 TCAGATCTATGGCCCTGTGGGAGTATN-----GACAGTGGCAATTTTCCACCT 2057

657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671

2058 GTAGCTATACCGACGACTCCCTGAAAGCGCTACATTGAGAACATTTTACCATTCCAAA 2117

672 -----MetGluArgAlaSerGlyLysThr 679

2118 CCAATGAGATGG-----CCATTTTCTTATTCACTTCTTCTTTATATTTCTTGTTGA 2171

680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696

2172 CTGATTCTATAATGGTGAAAGTTAAATTTCCAAAGGAAATAATCGAGAACTGAGGACTAT 2231

697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysIleTrpPheAlaLysGlu--- 714

2232 TCAAGCGATGAGCAACCTGAAAGTGAGAGTGAACTAAAGG 2273

715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 10

US-10-218-631-90

Sequence 90, Application US/10218631

Publication No. US20030045687A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3530P1C14

CURRENT APPLICATION NUMBER: US/10/218,631

CURRENT FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26


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Db 618 IleIleIleYalaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
Qy 1950 AATAACAAAAAGCACTGTCTACTGTAGTGCTTCATATTTACTCCAGATTGCTCAGTTCAA 2009
Db 637 AspSerArgAsnIleCysHisCysSerProGlyTyrIleCysProAsnCysGlnIleArg 656
Qy 2010 TCAGATCTATGGCTGGTGGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
Qy 2058 GTAGTATACAGCCAGACCTCCCTGAAAGCGCTACATTCAGAACATTTACCATTCACAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
Qy 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTCCTTCTTTATTTATTTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
Qy 2172 CTGATTCATTAATGGTGAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
Qy 2232 TCAAGCGATGAGCAACCTGAAAGTGAGAGTGAACCTAAAGCG 2273
Db 715 -----GluIlePheProSerSerGlySerGluGly 726

RESULT 11
US-10-230-414-90
; Sequence 90. Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 90
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
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Db 261 TrpLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaTyrLeuLeuIleTyrMet 280
Qy 885 GAAAGTCAAAATATGTTGGTCAACCTTTTCAAGGAGAGATGTGTGATGCAAACTATGCCA 944
Db 281 AspTyrProArgTyrLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
Qy 945 GGAGTGTGTTCTGACCCAGAACCAATAGTCTGGAATCACTTGGCAGTATTTTAGCT 1004
Db 301 AlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
Qy 1005 CAATTATTGAGCTTAGTATGGGATCACTTATCATGACATTAACAATGCCAGTGTCTCA 1064
Db 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCysGlnCysSer 340
Qy 1065 GGAGCTCTCTGCAATTATGAATCCAGAAGCAATTCATTTTCAGTGTGTGCAAGATCTTTAGT 1124
Db 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
Qy 1125 AACTGCAGCTTCGAGACTTTGCACATTTTATTTCAAGCAGAGTCCCGAGTGTCTTAC 1184
Db 361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
Qy 1185 AATCAGCTCGCTTAGATCTCTTTTCAACAGCAAGCAGTGTGTGTAATGCCAAAGCTG 1244
Db 381 AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
Qy 1245 GAAGCAGGAGGAGTGTGACTGTGGGACTGAACAGGATGTGCCCTTATTTGGAGAACA 1304
Db 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
Qy 1305 TGCTGTGATATTCGCCATGTAGATTTAAAGCCGGTTCAAACTGTGTGTGAAGCACCATGC 1364
Db 418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrLysGlyLeuCys 437
Qy 1365 TGGCAAACTCTCTATTATGTATGTCAAAAGAAAGATGTAGGCCT---TCTTTGAAGAA 1421
Db 438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
Qy 1422 TGGCACTCCCTCAATATTCGAATGGATCATCTGCATCATGCCAGCAAAACCACTATGTT 1481
Db 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
Qy 1482 CAGACTGGGATCCGCTGGAGCTGAATCAATGATCTGTATAGATGGAGTTGTATGAGT 1541
Db 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrAspGlyAspCysHisAsp 497
Qy 1542 GGGATAAACAATCTACAGACACATTTGGCAAGAGTATGTTGGCCCTTCAGATGT 1601
Db 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
Qy 1602 TATTCTCACCTTAATTCAAAGACTGTATCTGGAACCTGTGTATAAGT---GATTCA 1658
Db 518 TyrGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
Qy 1659 GGATACACACAGTGTGAAGCTGCAATCTCAGTGGCGGAAATTAATATGTAATATGTA 1718
Db 538 LysTyrValPheCysGlyTyrArgAsnLeuIleCysGlyArgLeuValCysThrTyrPro 557
Qy 1719 GGTAAATTTTATACAAATTCAGAGCCACTATTTATTTATGCAACATAAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
Qy 1779 CTCTGCATTCGTGGAAATTTGCCAGTGATCATGCAGCAGCCAAAGAGATGTGCATATAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
Qy 1839 GATGGAATCTCTGTGTTCAATAAGTTTGCAGGAATCAAGATGTGTGAGTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
Qy 1899 TACTTG-----GGTTATGATTGTACTACTGACAAATGCAATGATGATGAGTGTATGC 1949
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Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
QY 2058 GTAGCTATACCAAGCAGACTCCCTGAAAGCGCTACATTGAGAACATTTACCATTCACAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTCCTTCTTTATTTATTTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATTCGTATATGCTGAAAGTATTTCCAAAGGAGAAATCGAGACTGAGGACTAT 2231
Db 697 ---ThrThralaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
QY 2232 TCAAGCGATGAGCAACTGAAAGTGAGAGTGAACCTAAAGGG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726

RESULT 12

US-10-232-224-90
; Sequence 90, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C111
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 90
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-90

Alignment Scores:
Pred. No.: 3,87e-126 Length: 787
Score: 1524.50 Matches: 310
Percent Similarity: 58.89% Conservative: 134
Best Local Similarity: 41.11% Mismatches: 259
Query Match: 31.79% Indels: 51

DB: 14 Gaps: 18
US-10-054-683-18 (1-2640) x US-10-232-224-90 (1-787)
QY 72 ATGTGGTCTTGTCTCTCAGCGGCTCGGGGCTCGGATGCAC---AGTAATTTT 128
Db 4 LeutrPleu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe 21
QY 129 GATAGTTTACCTGTGCAAAATTACAGTTCGCGAGAAAATACGGTCAATAATAAAGAGGA 188
Db 22 GlnAenSerLeuLeuGlnIleValIleProGluLysIleGlnThrAenThrAenAspSer 41
QY 189 ATTGAA-----TCGAGGATCCTACAAAATTGTAATTGCAAGGAAAACCATATACT 239
Db 42 SerGluIleGluTyrGluGlnIleSerTyrIleIleProIleAspGluLysLeuTyrThr 61
QY 240 GTCAATTTAATGCAAAAACCTTTTACCCATAATTTTAGAGTTTACAGTTTACAGTTAGTGC 299
Db 62 ValHisLeuLysGlnArgTyrPheLeuAlaAspAsnPheMetIleTyrLeuTyrAsn--- 80
QY 300 ACAGGAATTTATGAAACCACTTGACCAAGATTTTTCAGAAATTTCTGCCACTACCAAGGGTAT 359
Db 81 GlnGlySerMetAsnThrTyrSerSerAspIleGlnThrGlnCysTyrTyrGlnGlyAsn 100
QY 360 ATTGAAGTTATCCAAAATCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 419
Db 101 IleGluGlyTyrProAspSerMetValThrLeuSerThrCysSerGlyLeuArgGlyIle 120
QY 420 CTACAGTTTGAATAATGTTAGTATGGAATAGAACCCCTGGAGCTTTCAGTTCGCTTGA 479
Db 121 LeuGlnPheGluAsnValSerTyrGlyIleGluProLeuGluSerAlaValGluPheGln 140
QY 480 CATGTAATTTACCAAGTAAACATAGAAAGCAGATGTTTCTCTATATATGTAATGAGGAT 539
Db 141 HisValLeuTyrLysLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer 160
QY 540 ATTGAATCAAGA-----GATCTGTCTCTTTAAATTAATAAGCCAGACGACACAGCAA 590
Db 161 LeuLysGluGlnProMetAspAsnIlePheIleSerGluLysSerGluProAlaVal 180
QY 591 GAT-----TTGCAAGTATATAGAAATGCGATGTTATAGTTGCAAAACATTTGTAAT 644
Db 181 ProAspLeuPheProLeuTyrLeuGluMetHisIleValValAspLysThrLeuTyrAsp 200
QY 645 CATATCGGTCTGATACAACTGTTGCGCTCAAAAGTTTTCAGTTGATTGATGATGACG 704
Db 201 TyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluIleValGlyLeuAla 220
QY 705 AATGCTATTTTGTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 764
Db 221 AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGluLeuTyrSer 240
QY 765 GATGAAAATTAATTCACACTGAGAGAACTAATGAGTATTACACATTTTAAAGA 824
Db 241 AspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuGlnLysPheLeuGlu 260
QY 825 TGGAAAACATCTTATCTGTTTACGCTCTCATGATGCGCATTTTCTTACTTGTGTTACAGA 884
Db 261 TrpLysGlnSerTyrLeuAsnLeuArgProHisAspIleAlaIleLeuLeuIleTyrMet 280
QY 885 GAAAAGTCAAAATTTATGTTGTCGAACCTTTCAAGGGAAGATGTTGATGCAAACTATGCA 944
Db 281 AspTyrProArgTyrLeuGluAlaValPheProGlyThrMetCysIleThrArgTyrSer 300
QY 945 GGAGGTGTTGTTCTGCACCCAGAACCAATAAGTCTCGAATCCTTGCAGTTATTTAGCT 1004
Db 301 AlaGlyValAlaLeuTyrProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
QY 1005 CAATTATTCAGCTTAGTATGGGATCCTTATGATGACATTAACAAATCCAGTGTCTCA 1064
Db 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrAspAspProLysLysCysGlnCysSer 340
QY 1065 GGAGCTGTCTGCATTTATGAATCCAGAACCAATTCATTTAGTGTGTGAAGATCTTTAGT 1124

Db 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
QY 1125 AACTGCAGCTCGAAGACTTTGCACATTTATTTTCAAGACGAGAGTCCCGAGTCTTCAC 1184
Db 361 SerCysSerLeuArgSerPheGlnAsnPhelSerAsnValGlyValLysCysLeuGln 380
QY 1185 AATCAGCTCGCTTAGATCTCTTTTCAAAACAGCAGCAGTGTGTGTAATGCAAGCTG 1244
Db 381 AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
QY 1245 GAACGACGAGAGAGTGTGACTGTGGGACTGAACAGGATGTGCTTATTTGGAGAAACA 1304
Db 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
QY 1305 TGCTGTGATATGTCACATAGATTTAAAGCCGGTCAAACTGTGCTGAGGACCATGC 1364
Db 418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysThrLysGlyLeuCys 437
QY 1365 TGCAGAACTGTCTATTATTATGTCAAAAGAAAGATGTAGGCT---TCTTTGAAAGAA 1421
Db 438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
QY 1422 TGGACCTCCCTGAATATTGCAATGATCATCTGCATCATGCCCCAGAAAACCATGTT 1481
Db 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
QY 1482 CAGACTGGCATCGCTGGACTCAATCAATGATGATGATGATGATGATGATGATGATGAT 1541
Db 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheLysCysThrAspGlyAspCysHisAsp 497
QY 1542 GGGGATAACAATGTACAGACACATTTGGCAAGAAAGATAGATGTTGGCCCTTCAGATGT 1601
Db 498 LeuAspAlaArgCysGluSerValPheGlyLysGlySerArgAsnAlaProPheAlaCys 517
QY 1602 TATTCTCACTTAATTCAGACAGTGTATCTCGAACTGTGTGTATAGT---GATTC 1658
Db 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
QY 1659 GGATACACACAGTGTGAAGCTGCAATCTGAGCGGAAATTAATATGTAATATGTA 1718
Db 538 LysThrValPheCysGlyThrArgAsnLeuIleCysGlyArgLeuValCysThrTyPro 557
QY 1719 GGTAAATTTTATTACAAATTCAGAGCCACTATTATTATGCAACATAAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrAlaPheValArgAspSer 577
QY 1779 CTCTGATCTGCTGGAAATTTGCCAGTGCATGCAGACAGCCMAAGATGTGATATAAA 1838
Db 578 ValCysIleThrValAspTyrLysLeuProArgThrValProAspProLeuAlaValLys 597
QY 1839 GATGGAACTTCTGTGTTCAATAAGCTTTGCAAGGAATCAAGATGTGTGAGTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
QY 1899 TACTTG-----GTTATGATTTGACTACAAATGCAATGCAATGATAGAGTGTATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
QY 1950 AATAACAAAAGACTGTCTACTGTAGTCTTCAATTTATTTACTCCAGATGCTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrLysProAsnCysGlnIleArg 656
QY 2010 TCAGATCTATGGCTGTGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluAspMetGlySerIle----- 671
QY 2058 GTAGCTATACAGCCAGACTCCCTGAAAGGCGCTACATTGAGAACATTTACCATTTCCAAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATGATGG-----CCATTTTCTTATTATCTCTTCTTCTTATTATTTCTGTGTA 2171

Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATTGCTATAATGGTGAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
QY 2232 TCAAGCGATGAGCAACTGAAAGTGAGAGTGAAACCTAAAGGG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726
RESULT 13
US-10-216-159A-90
; Sequence 90, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: P3530PIC6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 90
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-90
Alignment Scores:
Pred. No.: 3,87e-126 Length: 787
Score: 1524.50 Matches: 310
Percent Similarity: 58.89% Conservative: 134
Best Local Similarity: 41.11% Mismatches: 259
Query Match: 31.79% Indels: 51
DB: 14 Gaps: 18
US-10-054-683-18 (1-2640) x US-10-216-159A-90 (1-787)
QY 72 ATGTGGTCTTGTCTTCTGCTCAGCGGCTCGGCGGCTCGGATGAC---AGTAATTTT 128
Db 4 LeuTrpLeu-----LeuLeuAlaGlyLeuCysGlyLeuAlaSerArgProGlyPhe 21

Db 518 TyGluLueGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
Qy 1659 GGATACACACAGTGTGAAGCTGCAATCTCGAGTGGCGAAATTAATATGTAATGTA 1718
Db 538 LysTyValPheCysGlyTrpArgAsnLeuIleCysGlyArgLeuValCysThrTyPro 557
Qy 1719 GGTAAATTTTATACAAATTCGAAGCCACTATTTATGTCACATAAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyAlaPheValArgAspSer 577
Qy 1779 CTCTGCAATCTGTGGAAATTCGACAGTGATCATCCAGACAGCCAAAGATGTGATAAAA 1838
Db 578 ValCysIleThrValAspTyLysLeuProArgThrValProAspProLeuAlaValLys 597
Qy 1839 GATGGAATCTTCTGTGTTCAATAAGTTTGCAGGAATCAAGATGTGAGTTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
Qy 1899 TACTTG-----GGTTAGATTGTACTGACAAATGCAATGCAATGATAGAGGTGATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
Qy 1950 AATAACAAAAGCACTGCTACTGAGTCTTCATTTTACCTCCAGATTCGTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyLysProAsnCysGlnIleArg 656
Qy 2010 TCAGATCATGGCTGTGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluLysMetGlySerIle----- 671
Qy 2058 GTAGCTATACAGCCAGACTCCCTGAAAGCGGTACATTCAGAACACATTTACCATTCAAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
Qy 2118 CCAATGAGTGG-----CCATTTTCTTATTATTCCTCTTTTATTATTTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
Qy 2172 CTGATGCTATATGTTGGAAGTAAATTTCCAAAGGAAAAATGGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
Qy 2232 TCAAGCGATGAGCAACTGAAAGTGAGTGAACCTTAAGGG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerGluGly 726
RESULT 15
US-10-227-873-90
; Sequence 90, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; PRIOR FILING DATE: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
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; PRIOR FILING DATE: 1998-08-26
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; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Alignment Scores:

Pred. No.:	3 87e-126	Length:	787
Score:	1524.50	Matches:	310
Percent Similarity:	58.89%	Conservative:	134
Best Local Similarity:	41.11%	Mismatches:	259
Query Match:	31.79%	Indels:	51
DB:	14	Gaps:	18

US-10-054-683-18 (1-2640) x US-10-227-873-90 (1-787)

Qy	72	ATGTGGTCTGTGTTCTGTCTGACGGGCTCGGGGCTGGGATGAC---AGTAATTTT	128
Db	4	LeuTriPLeu-----LeuLeuAlaGlyLeuCysGlyLeuLeuAlaSerArgProGlyPhe	21
Qy	129	GATAGTTTACCTGTGCAAAATTACAGTTCGGGAGAAATACGGTCAATAATAAGGAAGGA	188
Db	22	GlnAsnSerLeuLeuGlnIleValIleProGluLysIleGlnThrAsnThrAsnAspSer	41
Qy	189	ATTGAA-----TCGCAGGCATCTACAAATTTGTAATTGAAGGGAACCATATACT	239
Db	42	SerGluIleGluTyroGluGlnIleSerTyroIleIleProIleAspGluLysLeuTyroThr	61
Qy	240	GTCAATTTAATGCAAAAAAATTTTACCCCATATAATTTAGAGTTTACAGTTTACAGTGGC	299
Db	62	ValHisLeuLysGlnArgTyroPheLeuAlaAspAsnPheMetIleTyroLeuTyroAsn--	80
Qy	300	ACAGGAATTATGAACCACTTGACCAAGATTTTCAGAAATTTCTGCCACTACCAAGGAT	359
Db	81	GlnGlySerMetAsnThrTyroSerSerAspIleGlnThrGlnCysTyroGlnGlyAsn	100
Qy	360	ATTGAAGGTTATCCAAAATCTGTGGTGGTTAGTGTAGTGTACTGTACTGAGTCTCAGGCGGTA	419
Db	101	IleGluGlyTyroProAspSerMetValThrLeuSerThrCysSerGlyLeuArgGlyIle	120
Qy	420	CTACAGTTTGAATAATCTTAGTTATGAATAGAACCCCTGGAGTCTTCAGTTCGCTTTGAA	479
Db	121	LeuGlnPheGluAsnValSerTyroGlyIleGluProLeuGluSerAlaValGluPheGln	140
Qy	480	CATGTAATTTACCAAGTAAACATAAGACGAGATGTTTCCCTTATATATAGAGAGGAT	539
Db	141	HisValLeuTyroLysLeuLysAsnGluAspAsnAspIleAlaIlePheIleAspArgSer	160

```
QY 540 ATTGAATCAAGA-----GATCTGCTCTTTAAATTACAAAGCGCAGAGCCACAGCAA 590
Db 161 LeuylsGluGlnProMetAspAspAsnIlePheIleSerGluylsValProAlaVal 180
QY 591 GAT-----TTTCAAAAGTATATAGAAATCATGTTATAGCTTCAAAACAAATGTATAAT 644
Db 181 ProAspLeuPheProLeuTyrlsLeuGluMetHisIleValValAspIlyThrLeuTyrlsAsp 200
QY 645 CATATGGGGTCTGATACAACTGTTGTGCTCAAAAAGTCTTTCAGTGTGATTGGATGACG 704
Db 201 TyrTrpGlySerAspSerMetIleValThrAsnLysValIleGluIleValGlyLeuAla 220
QY 705 AATGCTATTTTGTTCATTAATATATTAACAATTATCTGCTCTCAATGGAGCTTTGGATA 764
Db 221 AsnSerMetPheThrGlnPheLysValThrIleValLeuSerSerLeuGluLeuTrpSer 240
QY 765 GATGAAATAAATAATGCAACCACTGGAGAAAGCTAATGAGTTATTACACACATTTTAAAGA 824
Db 241 AspGluAsnLysIleSerThrValGlyGluAlaAspGluLeuGlnLysPheLeuGlu 260
QY 825 TGGAAACATCTTATCTTGTGTTTACGTCCTCATGATGTGCATTTTACTTGTTTACAGA 884
Db 261 TrpLysGlnSerTyrlsLeuAsnLeuArgProHisAspIleAlaTyrlsLeuLeuIleTyrlsMet 280
QY 885 GAAAGTCAAAATTTATGTTGTGTGCAACCTTTCAAGGGAGATGTGTGATGCAAACTATGCA 944
Db 281 AspTyrlsProArgTyrlsLeuGlyAlaValPheProGlyThrMetCysIleThrArgTyrlsSer 300
QY 945 GGAAGTGTCTTCTGCAACCCAGAACCAATAGCTGGAATCACTTGCAGTTATTTAGCT 1004
Db 301 AlaGlyValAlaLeuTyrlsProLysGluIleThrLeuGluAlaPheAlaValIleValThr 320
QY 1005 CAATATTAGACCTTAGTATGGGGATCACATTATGATGACATTAACAAATCCCAAGTCTCA 1064
Db 321 GlnMetLeuAlaLeuSerLeuGlyIleSerTyrlsAspAspProLysLysCysGlnCysSer 340
QY 1065 GGAAGTCTCTGCAATATGAAATCAGAAAGCAATTCATTTAGTGTGTGGAAGATCTTTAGT 1124
Db 341 GluSerThrCysIleMetAsnProGluValValGlnSerAsnGlyValLysThrPheSer 360
QY 1125 AACTGCAAGCTTCGAGACTTTGACATTTTATTTCAAGCAGAGTCCCAAGTCTCTTAC 1184
Db 361 SerCysSerLeuArgSerPheGlnAsnPheIleSerAsnValGlyValLysCysLeuGln 380
QY 1185 AATCAGCTCGCTTAGATCCCTTTTCAACAGCAAGCAGTGTGTGTAATGCAAAAGCTG 1244
Db 381 AsnLysProGlnMetGlnLys---LysSerProLysProValCysGlyAsnGlyArgLeu 399
QY 1245 GAACGAGGAGGAGGTGATGCTGTGGAGCTGAACAGAGTTGTGCCCTTATTTGGAGAAACA 1304
Db 400 GluGlyAsnGluIleCysAspCysGlyThrGluAlaGlnCysGly-----ProAlaSer 417
QY 1305 TGCTGTGATATTGCCATGATAGATTTAAAGCCGTTCAACTGTGCTGAAGGACCATGC 1364
Db 418 CysCysAspPheArgThrCysValLeuLysAspGlyAlaLysCysTyrlsGlyLeuCys 437
QY 1365 TGGCAAACTGCTATTATTATCAAAAGAAAGTGTAGGCT---TCCTTTGAAGAA 1421
Db 438 CysLysAspCysGlnIleLeuGlnSerGlyValGluCysArgProLysAlaHisProGlu 457
QY 1422 TGGACCTCCCTGAATATGCAATGGAATCATCTGATCATGCCAGAAACCACTATGTT 1481
Db 458 CysAspIleAlaGluAsnCysAsnGlySerSerProGluCysGlyProAspIleThrLeu 477
QY 1482 CAGACTGGGATCCGTTGGAGCTGAATCAATGATCTGTATAGATGGAGTTTGTATGAGT 1541
Db 478 IleAsnGlyLeuSerCysLysAsnAsnLysPheIleCysTyrlsAspGlyAspCysHisAsp 497
QY 1542 GGGATAAACAATGTACAGACACATTTGGCAAGAAAGTACAGATTGTGGCCCTTCAGAAATGT 1601
Db 498 LeuAspAlaArgCysGluSerValPheGlyIleGlySerArgAsnAlaProPheAlaCys 517
QY 1602 TATTCTCACCTTAATCAAGAGCTGATGTATCTCGAAACCTGTGGTATAAGT---GATTCA 1658
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Db 518 TyrGluGluIleGlnSerGlnSerAspArgPheGlyAsnCysGlyArgAspArgAsnAsn 537
QY 1659 GGATACACACAGGTGCTGAAGCTGACAATCTGCAGTGGGAAAAATTAATATGTAATATGTA 1718
Db 538 LysTyrlsValPheCysGlyTrpArgAsnLeuIleCysGlyArgLeuValCysThrTyrlsPro 557
QY 1719 GGTAAATTTTATTACAAATTTCAAGAGCCACTATTATTATGCCAACATAAGTGGACAT 1778
Db 558 ThrArgLysProPheHisGlnGluAsnGlyAspValIleTyrlsAlaPheValArgAspSer 577
QY 1779 CTCTGCATTTCTGTGGAATTTGGCAGTGCATCATGCAGACAGCCAAAGATGTCGATAAA 1838
Db 578 ValCysIleThrValAspTyrlsLeuProArgThrValProAspProLeuAlaValLys 597
QY 1839 GATGGAATCTTCTGTGTTGTTCAATAAGTTTGCAGGAATCAAAAGATGCTGTGAGTCTTCA 1898
Db 598 AsnGlySerGlnCysAspIleGlyArgValCysValAsnArgGluCysValGluSerArg 617
QY 1899 TACTTG-----GGTTATGATTGTACTACTGCAAAATGCAATGCAATGATAGAGTGTATGC 1949
Db 618 IleIleLysAlaSerAlaHisValCys---SerGlnGlnCysSerGlyHisGlyValCys 636
QY 1950 AATAACAAAAGCACTGTCACTGCTGCTTCAATATTACCTCCAGATTCCTCAGTTCAA 2009
Db 637 AspSerArgAsnLysCysHisCysSerProGlyTyrlsProAsnCysGlnIleArg 656
QY 2010 TCAGATCTATGGCTGCTGGAGTATT-----GACAGTGGCAATTTTCCACCT 2057
Db 657 Ser-----LysGlyPheSerIlePheProGluGluAspMetGlySerIle----- 671
QY 2058 GTAGCTATACAGCCAGACTCCCTGAAAGCGCTACATTGAGAACATTTTACCATTCCAA 2117
Db 672 -----MetGluArgAlaSerGlyLysThr 679
QY 2118 CCAATGAGATGG-----CCATTTTCTTATTCATTCCTTCTTTTATTATTCTGTGTA 2171
Db 680 GluAsnThrTrpLeuLeuGlyPheLeuIleAlaLeuProIleLeuIleVal----- 696
QY 2172 CTGATTGCTATAATGTTGAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTAT 2231
Db 697 ---ThrThrAlaIleValLeuAlaArgLysGlnLeuLysLysTrpPheAlaLysGlu--- 714
QY 2232 TCAAGCGCATGAGCAACCTGAAAGTGAAGTGAAGTGAACCTAAAGGG 2273
Db 715 -----GluGluPheProSerSerGluSerLysSerLysSerGluGly 726
```

Search completed: January 10, 2005, 22:20:41
Job time : 396.5 secs

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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:47:51 ; Search time 160 Seconds
(without alignments)
1645.671 Million cell updates/sec

Title: US-10-054-683-19

Perfect score: 3984

Sequence: 1 MWYFLSLGLGLRMSNFD.....WRTEYSDQPESESEPKG 734

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Genesep_23Sep04:.*
1: Genesep1980s:.*
2: Genesep1990s:.*
3: Genesep2000s:.*
4: Genesep2001s:.*
5: Genesep2002s:.*
6: Genesep2003as:.*
7: Genesep2003bs:.*
8: Genesep2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3984	100.0	734	2 AAR87037	Aar87037 Human PH3
2	3984	100.0	734	6 ABJ19246	Abj19246 Human can
3	3984	100.0	734	7 ADB75186	Adb75186 Prostate
4	3969.5	99.6	735	7 ADB75184	Adb75184 Prostate
5	3898	97.8	753	7 ADB75182	Adb75182 Prostate
6	3551	89.1	651	2 AAR87034	Aar87034 Human PH3
7	2440	61.2	735	2 AAR87036	Aar87036 Mouse PH3
8	1524.5	38.3	787	5 AAU83636	Aau83636 Human PRO
9	1524.5	38.3	787	6 ABU80783	Abu80783 Human PRO
10	1524.5	38.3	787	6 ABO33749	Abo33749 Novel hum
11	1524.5	38.3	787	6 ABU82092	Abu82092 Novel hum
12	1524.5	38.3	787	6 ABJ72272	Abj72272 Human PRO
13	1524.5	38.3	787	6 ABJ72400	Abj72400 Human PRO
14	1524.5	38.3	787	6 ABO34295	Abo34295 Human sec
15	1524.5	38.3	787	7 ABJ72102	Abj72102 Human mem
16	1524.5	38.3	787	7 ADB83580	Adb83580 Novel hum
17	1524.5	38.3	787	7 ADB80686	Adb80686 Novel hum
18	1524.5	38.3	787	7 ADB73227	Adb73227 Novel hum
19	1524.5	38.3	787	7 ADB78309	Adb78309 Novel hum
20	1524.5	38.3	787	7 ADB84957	Adb84957 Human PRO
21	1524.5	38.3	787	7 ADB78063	Adb78063 Novel hum
22	1524.5	38.3	787	7 ADB87129	Adb87129 Human PRO
23	1524.5	38.3	787	7 ADB84711	Adb84711 Human PRO
24	1524.5	38.3	787	7 ADB83826	Adb83826 Novel hum
25	1524.5	38.3	787	7 ADB72981	Adb72981 Novel hum

26	1524.5	38.3	787	7 ADC36819	Adc36819 Human PRO
27	1524.5	38.3	787	7 ADC21809	Adc21809 Human PRO
28	1524.5	38.3	787	7 ADC49840	Adc49840 Novel hum
29	1524.5	38.3	787	7 ADC49039	Adc49039 Novel hum
30	1524.5	38.3	787	7 ADC49556	Adc49556 Novel hum
31	1524.5	38.3	787	7 ADC47417	Adc47417 Novel hum
32	1524.5	38.3	787	7 ADC47162	Adc47162 Novel hum
33	1524.5	38.3	787	7 ADC78037	Adc78037 Novel hum
34	1524.5	38.3	787	7 ADD06272	Add06272 Novel hum
35	1524.5	38.3	787	7 ADC77791	Adc77791 Novel hum
36	1524.5	38.3	787	7 ADD50754	Add50754 Novel hum
37	1524.5	38.3	787	7 ADD51000	Add51000 Novel hum
38	1524.5	38.3	787	7 ADD50481	Add50481 Human PRO
39	1524.5	38.3	787	7 ADD50235	Add50235 Human PRO
40	1524.5	38.3	787	7 ADD51246	Add51246 Novel hum
41	1524.5	38.3	787	8 ADC48793	Adc48793 Novel hum
42	1524.5	38.3	787	8 ADE20964	Ade20964 Novel hum
43	1524.5	38.3	787	8 ADE05808	Ade05808 Human PRO
44	1524.5	38.3	787	8 ADD75037	Add75037 Human PRO
45	1524.5	38.3	787	8 ADD75783	Add75783 Novel hum

ALIGNMENTS

RESULT 1
AAR87037
ID AAR87037 standard; protein; 734 AA.
XX AAR87037;
XX
DT 30-SEP-1996 (first entry)
XX
DE Human PH30 beta chain sperm protein.
XX
KW Human PH30 beta chain sperm protein; contraceptive;
KW FEE integrin binding domain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 84..734
FT /note= "see AAR87035"
XX
PN WO9535118-A1.
PD 28-DEC-1995.
XX
PF 06-JUN-1995; 95WO-US007295.
XX
PR 20-JUN-1994; 94US-00264101.
XX
PA (MERI) MERCK & CO INC.
XX
PI Alves K, Gupta SK, Hollis GF;
XX WPI; 1996-058212/06.
XX N-PSDB; AAT07329.
XX
FT Human and mouse sperm protein PH30 beta chain and related DNA - useful in
FT contraceptive vaccines.
XX
PS Example 2; Page 45-48; 85pp; English.
XX
CC Human PH30 beta chain sperm protein, having a FEE integrin binding
CC domain, is 58.9% identical to mouse and 56.5% identical to guinea pig
CC PH30 beta. The protein may be produced recombinantly and used in a
CC contraceptive composition containing an effective adjuvant and an amount
CC of sperm protein which is effective for the stimulation of antibodies
CC which bind to sperm protein in vivo, thereby preventing or substantially
CC reducing the rate of sperm-egg fusion
XX
SQ Sequence 734 AA;

```
Query Match      100.0%; Score 3984; DB 2; Length 734;
Best Local Similarity 100.0%; Pred. No. 5.5e-292;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWVLLSGLGRLMDSNFDLPVQITVPEKIRIIKEGIESQASYKIVIEGKPYTVNLM 60
Db 1 MWVLLSGLGRLMDSNFDLPVQITVPEKIRIIKEGIESQASYKIVIEGKPYTVNLM 60
Qy 61 QKNFLPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGLQFE 120
Db 61 QKNFLPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGLQFE 120
Qy 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQDFAKYIE 180
Db 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQDFAKYIE 180
Qy 181 MHVIVEKQLYNHMGSDTTVAQKVFQILGTNAIFVSNITIISSLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQKVFQILGTNAIFVSNITIISSLELWIDENKIATTG 240
Qy 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFQGMKCDANVAGGVVLPRT 300
Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFQGMKCDANVAGGVVLPRT 300
Qy 301 ISLESVAVILAQLLSLWIGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360
Db 301 ISLESVAVILAQLLSLWIGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360
Qy 361 FISKQKSOCLHNPRLDPPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
Db 361 FISKQKSOCLHNPRLDPPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
Qy 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQ 480
Db 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQ 480
Qy 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLIKCVYKFLQIPRATIIYANISGHLCAIEAFADSHADSKQMWIKDGTSCGSKVC 600
Db 541 CGKLIKCVYKFLQIPRATIIYANISGHLCAIEAFADSHADSKQMWIKDGTSCGSKVC 600
Qy 601 RNQRCVSSSYLYDCTTDKNDRGVCNKKHCHCSASYLPDSCSVQSDLPFGGSDISGNF 660
Db 601 RNQRCVSSSYLYDCTTDKNDRGVCNKKHCHCSASYLPDSCSVQSDLPFGGSDISGNF 660
Qy 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFPFFIIFCVLIAIMVKNVFORKKWRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFPFFIIFCVLIAIMVKNVFORKKWRTEDY 720
Qy 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734

RESULT 2
ABU19246
ID ABU19246 standard; protein; 734 AA.
XX
AC ABU19246;
DT 28-MAR-2003 (first entry)
XX
DE Human cancer/testis antigen - SEQ ID No 19.
XX
KW Human; gene therapy; vaccine; cancer; cancer/testis antigen; CT antigen.
XX
OS Homo sapiens.
XX
PN W0200278526-A2.
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XX 10-OCT-2002.
XX 29-MAR-2002; 2002WO-US009808.
XX 30-MAR-2001; 2001US-0280718P.
PR 20-APR-2001; 2001US-0285154P.
PR 05-OCT-2001; 2001US-0327432P.
XX 22-JAN-2002; 2002US-00054683.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (CORR ) CORNELL RES FOUND INC.
XX
XX Old Lj, Scanlan MJ, Chen Y;
XX WPI; 2003-040608/03.
DR N-PSDB; ABT15727.
XX
XX Diagnosing cancer comprises contacting a biological sample isolated from
PT a subject with an agent that specifically binds to a nucleic acid
PT molecule, its expression product or fragment or an antibody that binds to
PT the product or fragment.
XX
XX Claim 36; Page 124-126; 155pp; English.
XX
XX The invention comprises a method for diagnosing cancer, the method
CC involves detecting the DNA or protein sequences of human cancer/testis
CC (CT) antigens that are disclosed in the invention. The method of the
CC invention is useful for detecting/diagnosing, treating and monitoring a
CC cancer or condition characterised by the expression of a human CT
CC antigen. The present amino acid sequence represents a human CT antigen of
CC the invention
XX
XX Sequence 734 AA;
```

```
Query Match      100.0%; Score 3984; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 5.5e-292;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWVLLSGLGRLMDSNFDLPVQITVPEKIRIIKEGIESQASYKIVIEGKPYTVNLM 60
Db 1 MWVLLSGLGRLMDSNFDLPVQITVPEKIRIIKEGIESQASYKIVIEGKPYTVNLM 60
Qy 61 QKNFLPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGLQFE 120
Db 61 QKNFLPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGLQFE 120
Qy 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQDFAKYIE 180
Db 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQDFAKYIE 180
Qy 181 MHVIVEKQLYNHMGSDTTVAQKVFQILGTNAIFVSNITIISSLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQKVFQILGTNAIFVSNITIISSLELWIDENKIATTG 240
Qy 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFQGMKCDANVAGGVVLPRT 300
Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFQGMKCDANVAGGVVLPRT 300
Qy 301 ISLESVAVILAQLLSLWIGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360
Db 301 ISLESVAVILAQLLSLWIGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360
Qy 361 FISKQKSOCLHNPRLDPPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
Db 361 FISKQKSOCLHNPRLDPPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
Qy 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQ 480
Db 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQ 480
Qy 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
```


Db 481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLSKNTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLICKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Db 541 CGKLICKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Qy 601 RNORCVSSSYLGVDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLWPGSGIDSNGF 660
Db 601 RNORCVSSSYLGVDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLWPGSGIDSNGF 660
Qy 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIFCVLIAIMVKVNFQKWKRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIFCVLIAIMVKVNFQKWKRTEDY 720
Qy 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734

RESULT 3
ADB75186
ID ADB75186 standard; protein; 734 AA.
AC ADB75186;
XX
XX 04-DEC-2003 (first entry)
DE Prostate cancer marker protein.
XX
XX Prostate; cancer; cytostatic; gene therapy; marker.
OS Homo sapiens.
XX
XX WO2003009814-A2.
XX
XX 06-FEB-2003.
XX
XX 25-JUL-2002; 2002WO-US023913.
XX
XX 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Schlegel R, Monahan JF, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
XX WPI; 2003-248033/24.
XX
XX New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
XX
XX Disclosure; SEQ ID NO 10; 99pp; English.
XX
XX The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 734 AA;
Query Match 100.0%; Score 3984; DB 7; Length 734;
Best Local Similarity 100.0%; Pred. No. 5.5e-292;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MWVLFLLSGGLGRMDSNFDLSPVQITVPEKIRSIIEGIESQASVKIVIEGPKYTVNLM 60
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Db 61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGLQFE 120
Qy 121 NVSYGIEPLESSVGFHVIYQVHKADVSLYNEKDIERSDLSPKQASBPQDFAKYIE 180
Db 121 NVSYGIEPLESSVGFHVIYQVHKADVSLYNEKDIERSDLSPKQASBPQDFAKYIE 180
Qy 181 MHVIVEKQLYNHMGSDTTVAQVQFOLIGITNAIFVSFNITIISSLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQVQFOLIGITNAIFVSFNITIISSLELWIDENKIATTG 240
Qy 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVVGATFOGKMCADANYAGGVVLHPT 300
Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVVGATFOGKMCADANYAGGVVLHPT 300
Qy 301 ISLESALVILAQLLSLMSGITDYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360
Db 301 ISLESALVILAQLLSLMSGITDYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSFEDFAH 360
Qy 361 FISKQKSQCLHNQPRLDPPFKQAVCGNAKLEAGEECDCGTEODCALIGETCCDIATCRF 420
Db 361 FISKQKSQCLHNQPRLDPPFKQAVCGNAKLEAGEECDCGTEODCALIGETCCDIATCRF 420
Qy 421 KAGSNCAEGPCCBCLFMSKERMCRPSFECDDLPEYCNSSSASCENHYVQTGHPCGLNQ 480
Db 421 KAGSNCAEGPCCBCLFMSKERMCRPSFECDDLPEYCNSSSASCENHYVQTGHPCGLNQ 480
Qy 481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLSKNTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLSKNTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLICKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Db 541 CGKLICKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Qy 601 RNORCVSSSYLGVDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLWPGSGIDSNGF 660
Db 601 RNORCVSSSYLGVDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLWPGSGIDSNGF 660
Qy 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIFCVLIAIMVKVNFQKWKRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIFCVLIAIMVKVNFQKWKRTEDY 720
Qy 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734

RESULT 4
ADB75184
ID ADB75184 standard; protein; 735 AA.
XX
XX ADB75184;
AC ADB75184;
XX
XX 04-DEC-2003 (first entry)
DE Prostate cancer marker protein.
XX
XX Prostate; cancer; cytostatic; gene therapy; marker.
XX
XX Homo sapiens.
XX


```

Db 422 FGPSECYSHLSKSTVDSNGCISDSGYTQCADNLQCGKLCXYGKFLQIPRATIIYA 481
Qy 565 NISGHLCIAVEFADHADSOQMWIKDGTSCSNKVCNQRQVSSSYLGDCCTTKCNDRG 624
Db 482 NISGHLCIAVEFADHADSOQMWIKDGTSCSNKVCNQRQVSSSYLGDCCTTKCNDRG 541
Qy 625 VCNKKGCHCSASYLPDPCSVQSDLPWPGGSDSGNFPFPAIPARLPERRYIENIYHSPM 684
Db 542 VCNKKGCHCSASYLPDPCSVQSDLPWPGGSDSGNFPFPAIPARLPERRYIENIYHSPM 601
Qy 685 RWPFFLPFPIIFCVLIAIMVKNFQKWKRTEDYSSDEQPESESEPKG 734
Db 602 RWPFFLPFPIIFCVLIAIMVKNFQKWKRTEDYSSDEQPESESEPKG 651

RESULT 7
AAR87036
ID AAR87036 standard; protein; 735 AA.
XX
AC AAR87036;
DT 30-SEP-1996 (first entry)
XX
DE Mouse PH30 beta chain sperm protein.
XX
KW Mouse PH30 beta chain sperm protein; contraceptive;
KW ODE integrin binding domain.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 279..735
FT /note= "see AAR87035"
XX
EN WO9535118-A1.
XX
PD 28-DEC-1995.
XX
PF 06-JUN-1995; 95WO-US007295.
XX
PR 20-JUN-1994; 94US-00264101.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Alves K, Gupta SK, Hollis GF;
XX
PT WPI; 1996-058212/06.
XX
DR N-PSDB; AAT07327.
XX
Human and mouse sperm protein PH30 beta chain and related DNA - useful in
contraceptive vaccines.
XX
PS Example 2; Page 39-41; 85pp; English.
XX
CC Mouse PH30 beta chain sperm protein, having a QDE integrin binding
CC domain, is 55.2% identical to guinea pig PH30 beta. The protein may be
CC produced recombinantly and used in a contraceptive composition containing
CC an effective adjuvant and an amount of sperm protein which is effective
CC for the stimulation of antibodies which bind to sperm protein in vivo,
CC thereby preventing or substantially reducing the rate of sperm-egg fusion
XX
SQ Sequence 735 AA;

Query Match 61.2%; Score 2440; DB 2; Length 735;
Best Local Similarity 59.6%; Pred. No. 2.6e-175;
Matches 439; Conservative 119; Mismatches 167; Indels 12; Gaps 7;

Qy 3 VLFLLSG---LGGL---RMDNFDPSLPVQITVPEKIRSIKEGIESQASQKIVIEGKPYT 56
Db 4 ILLLLSGELGGLSQSGTEGTRKXHVQVTVPEKIRSVTSNGYETQVYNLKEGKTYT 63
Qy 57 VNLMOKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYGQYIEGYPKSVVMVSTCTGLRGV 116

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Db 64 LDLMQKFPDPNFRVSYDNAGIMRSLERQFQNICYFQGYIEGYPSNWMVISTCTGLRGF 123
Qy 117 LQPNWVSYGTEPLESSVGFVHVYQVGHKKADVSLYNEKDIESTDLSEFKLSQAPQDDFA 176
Db 124 LQFNWVSYGTEPLESSVGFVHVYQVPEKGGALLYAEKIDLDLDSYKIRSIKQIRVS 183
Qy 177 KYIEMHVIVKQLNYNHMGSDTTVVAAQVFLQIGLTNAIFVSFNITIIISLSLELWIDENKI 236
Db 184 HYLEIHIVVEKQMFHEHIGADTAIVTQKIFQIGLANAIFAPFNLTVILSSLEFWMENKI 243
Qy 237 ATTCEANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYGATFQGMCDANDYAGGVVL 296
Db 244 LTTGDANKLJYRFLKWKQSYLVLRPHDMAFLVYRNTTDYVGYTQGMCDKNYAGGVVL 303
Qy 297 HPTISLESIAVILAQLLSLSMGITDDINKCCSGAVCIMNPEAIHFSGVKIFSNCSFE 356
Db 304 HPKAVTLESIAVILVQLLSLMLAYDDVNNKCCGVPCVMNPEAPHSSGVRAFSNCSME 363
Qy 357 DFAHFISKQKSCQLHNQPRLDFFKQAAVCGNAKLEAGEECDCGTEQDCALIGTCCDIA 416
Db 364 DFSKFITSSQSHCLQNOPTLQPSYK-MAVCGNGEVEBEICDQG-KKGCAEMPPPCNP 421
Qy 417 TCRFKAGSNCAEGPCCECLFMSKERMCRSFEBCLDLPYCNCGSSASCENHYVOTGHP 476
Db 422 TKLSLDGSECSGICCNCKLKRKEVCRLAQDECDVTEYCNGTSEVC-EDFFVQNGHPC 480
Qy 477 GLNQWICIDGVCMSGDKQCTDTFGKEVFGPSECYSHLSKSTVDSNGCISDSGYTCEA 536
Db 481 DNRKWICINTCSGEGEQCDLFGIDAGFSSECFWELNSKSDISGCGISAGYKCEPP 540
Qy 537 DNLQCGKLI CKYVGKFLQIPRATIIYANISGHLCIAVEFADHADSOQMWIKDGTSCGS 596
Db 541 NDRMCGKII CKYQSENILKRSATVIYANISGHVCSLEYVPGHNSQKMWVRDGTVCGS 600
Qy 597 NKVCRNORCVSSSYLGDCCTDKNDRGVCNKKHCHCSASYLPDPCSVQSDLPWPGGSD 656
Db 601 NKVCQKQKCVADTFLGYDCNLEKCNHHGVCNKKCHCDPTLPPDCRKMKDSYPGGSD 660
Qy 657 SGNFPFPAIPARLPERRYIENIYHSPKMRWPFFLPFPIIFCVLIAIMVKNFQKWK 716
Db 661 SGN-KERAEP--IPVRPIASRYRSKSPRWPFFLPFPIIFVYVILVILGLVKVYSQRMK 717
Qy 717 TEDYSDEQPESESEPK 733
Db 718 MDDFSSEEQFESESEK 734

RESULT 8
AAU83636
ID AAU83636 standard; protein; 787 AA.
XX
AC AAU83636;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 90.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
EN W0200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.

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Db 241 DENKISTVGEADELLOKLEWQSYLNLRPHDIAYLLIYMDYPRYLGAVPFGTMCITRYS 300
Qy 292 GGVVLPRTISLESVLAIAQLLSMGITVDDINKCQCSGAVCINWPEAHFSGVKIPS 351
Db 301 AGVALYKEITLEAFVIVTQMLALSIGISYDDPKCCQSESTCINWPEVVGNGVKTF 360
Qy 352 NCSFEDFAHFISKQSOCLNRPDLDPFFKQAVCGNAKLEAGEECDCGTEQCALIGET 411
Db 361 SCSLSRFQNFISNVGVKCLQNKQMQK-KSPKPCVCGNRLGEGNEICDCGTEACG--PAS 417
Qy 412 CDDIATCRFAGSNCAEGPCCNCLFMSKERMCRP-SFEECDLPEYNGSSASCENHYV 470
Db 418 CCDFRITCVLKGAKYKGLCKDCQILQSGVECRPKAHPEDCIAENCGSSPCCGPDITL 477
Qy 471 QTGHPCGLNQCICIDGVMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529
Db 478 INGLSKNNKFIICYDGDCHDLDAECESVFGKSRNAPFACYEIQSQDRFGNCGDRNN 537
Qy 530 GYTQCEADNLQCGKLIQKLVGKFLQIPRATIIYANISGHLCAVEFASDHADSRQMWIK 589
Db 538 KYVFCGWRNLICGLVCTYTRKPFHQENGDIYAFVRDSVCITVDYKLPRTVPDPLAVK 597
Qy 590 DGTSCGSKNVCNRCORCVSSYL---GYDCTTDKNDRGVNCNKKHCHCSASYLPDPCSVQ 646
Db 598 NGSQCDIGRVCNRECVESRIIKASAHVC-SQCSGHGVCDNRKCHCSPGYKPPNCQIR 656
Qy 647 SLDWPGCSI-----DSGNFPFVAIPARLPERRYENIYHSPMRW--PFFLFIFFFI 700
Db 657 S---KGFSIPPEEDMGSI-----MERASGKTENTWLLGLFIALPILIV--- 696
Qy 701 LIAIMKVNFORKKWRTEDYSSDEQSESEPKG 734
Db 697 -TTAIVLARKQLKWKFAKE---EEFPSSSEKSEG 726

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RESULT 12

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ABJ72272
ID ABJ72272 standard; protein; 787 AA.
XX ABJ72272;
XX
XX 06-NOV-2003 (first entry)
XX Human PRO21340 protein.
XX
XX PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
XX differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX
XX Homo sapiens.
XX
XX US2003050448-A1.
XX
XX 13-MAR-2003.
XX
XX 28-AUG-2002; 2002US-00230414.
XX
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-521818/49.
XX N-PSDB; ABT44270.
XX
XX New nucleic acid encoding for a PRO protein, useful for the manufacture
XX of a medicament for diagnosing or treating tumors or for measuring or
XX detecting expression of an associated gene.
XX

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Claim 11; Fig 90; 315pp; English.

The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TNF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or differentiation, the stimulation of human dermal fibroblast cell proliferation, and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention

SQ Sequence 787 AA;

Query Match 38.3%; Score 1524.5; DB 6; Length 787;
 Best Local Similarity 41.1%; Pred. No. 4.3e-106;
 Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18;

```

Qy 1 MVLPLSLGLGLRMD-SNFDLPLVQITVPEKIRSIKEGIE---SQASYKIVIEGKPYT 56
Db 4 LML--LLAGLCGLLASRPGFQNSLQIVPEKIQTNWDSSEIEYQISYIIPIDEKLYT 61
Qy 57 VNLMQNPLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQYIEGYKSVVMVSTCTGLRGV 116
Db 62 VHLKQRYFLADNFMILYN-QGSMNTYSSDIQTQCYQCNIEGYPDSMTLSTCSGLGI 120
Qy 117 LQENVSYGIEPLESSVGFHEVIYQVKKKADVSLNEXKDIESR---DLSFKLOSREPQQ 173
Db 121 LQENVSYGIEPLESSVGFHEVIYQVKKKADVSLNEXKDIESR---DLSFKLOSREPQQ 180
Qy 174 D--FAKVIEMHIVKOLYNHMGSDTTVAQVQFQILGLTNAIFVSFNITILSSLELWI 231
Db 181 PDLFPLYLEWHIVVDKLYDYGSDSNITNKNVIEIVGLANSFTQFKTIVLSSLELWS 240
Qy 232 DENKIATTEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGFATQGGKCDANYA 291
Db 241 DENKISTVGEADELLOKLEWQSYLNLRPHDIAYLLIYMDYPRYLGAVPFGTMCITRYS 300
Qy 292 GGVVLPRTISLESVLAIAQLLSMGITVDDINKCQCSGAVCINWPEAHFSGVKIPS 351
Db 301 AGVALYKEITLEAFVIVTQMLALSIGISYDDPKCCQSESTCINWPEVVGNGVKTF 360
Qy 352 NCSFEDFAHFISKQSOCLNRPDLDPFFKQAVCGNAKLEAGEECDCGTEQCALIGET 411
Db 361 SCSLSRFQNFISNVGVKCLQNKQMQK-KSPKPCVCGNRLGEGNEICDCGTEACG--PAS 417
Qy 412 CDDIATCRFAGSNCAEGPCCNCLFMSKERMCRP-SFEECDLPEYNGSSASCENHYV 470
Db 418 CCDFRITCVLKGAKYKGLCKDCQILQSGVECRPKAHPEDCIAENCGSSPCCGPDITL 477
Qy 471 QTGHPCGLNQCICIDGVMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529
Db 478 INGLSKNNKFIICYDGDCHDLDAECESVFGKSRNAPFACYEIQSQDRFGNCGDRNN 537
Qy 530 GYTQCEADNLQCGKLIQKLVGKFLQIPRATIIYANISGHLCAVEFASDHADSRQMWIK 589
Db 538 KYVFCGWRNLICGLVCTYTRKPFHQENGDIYAFVRDSVCITVDYKLPRTVPDPLAVK 597
Qy 590 DGTSCGSKNVCNRCORCVSSYL---GYDCTTDKNDRGVNCNKKHCHCSASYLPDPCSVQ 646
Db 598 NGSQCDIGRVCNRECVESRIIKASAHVC-SQCSGHGVCDNRKCHCSPGYKPPNCQIR 656
Qy 647 SLDWPGCSI-----DSGNFPFVAIPARLPERRYENIYHSPMRW--PFFLFIFFFI 700
Db 657 S---KGFSIPPEEDMGSI-----MERASGKTENTWLLGLFIALPILIV--- 696
Qy 701 LIAIMKVNFORKKWRTEDYSSDEQSESEPKG 734
Db 697 -TTAIVLARKQLKWKFAKE---EEFPSSSEKSEG 726

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polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
 Claim 19; Fig 90; 315pp; English.

The invention relates to an isolated nucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate full length PRO cDNA. The PRO polypeptides are useful for chondrocyte stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an animal. The PRO polypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents the amino acid sequence of a human secreted/transmembrane PRO polypeptide

Sequence 787 AA;

Query Match 38.3%; Score 1524.5; DB 6; Length 787;
 Best Local Similarity 41.1%; Pred. No. 4.3e-106;
 Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18;

QY 1 MWVFLSLGSGGLRMD-SNFDSPVQITPEKIRSIKEGIE---SQASKVIIEGKPYT 56
 DB 4 LWL--LLAGLCGLASRPGFQNSLLQIVPEKIQTNTDSIEYEIQIYIPIDEKLYT 61

QY 57 VNLMOXNLFPHNRVSYSGTGIMKPLDQDFQFCHQYVIEGPKSVVMVSTCTGLGV 116
 DB 62 VHLKQRYFLADNFMVLYLN-QGSNNTYSDDIQYQYQYVIEGPKSVVMVSTCTGLGV 120

QY 117 LQFENSYGIEPLESSVGFHEVIVQVKKADVSLYNEKIDIESR---DLSEFKLQSAEPQ 173
 DB 121 LQFENSYGIEPLESAVEFQVLYLKLKEDNDIAIFIDRSLSKQPMDDNIFISEKSEPAV 180

QY 174 D--FAKYIEMHIVIEKOLNHNMGSDTTVAQKVPQLIGLNTAIPVSNITIIISLLEWI 231
 DB 181 PDLFPYLEHIVVDKTLVDYWGSDSMIVTNKVIIEVGLANSMTQPKVIVLSSLEWS 240

QY 232 DENKIATGANEHLHTFLRWKSYLVLRHDVLAFLAVREKSNYVCATQFGKMCNDAYA 291
 DB 241 DENKISTVGEADELLQFLWKQSYLVLRHDVLAFLAVREKSNYVCATQFGKMCNDAYA 300

QY 292 GGVVLPRTISLESIAVLAQLISLGMITVDDINKQCQSGAVCIMNPEAIHFSGVKIFS 351
 DB 301 AGVALYKPEITLEAFVIVTQMLALSLSIGSYDDPKKQCSSESTCIMNPEVQVNGVKTFS 360

QY 352 NCSFEDFAHFIISKQSLNHNQPLDFFQKQAVGNKAEAGECDGTEQDCALIGET 411
 DB 361 SCSLRSQNFISNVGVKCLQNKQPMQK-KSPKPVCGNGLRGNIEICDQTEAQCQ--PAS 417

QY 412 CDDIATCRFKAGSCAGPCENCLFMSKEMCRP-SFECDLPEYCNCGSSASCENHYV 470
 DB 418 CDDPRTVLDKAGKYKGLCKDCQIQLQSGVECHPKAHPEDIAENCGSPGCPDITL 477

QY 471 QTGHPCGLNQCICDGVCMGSDKQCTDTFGKEVFGPSECVSHLNSKTDVSGNGIS-DS 529
 DB 478 INGLSKNNKFEICVDGCHDLDAECESVFGKSRNAPACVYEETQSQDRFGNCGDRNN 537

QY 530 GYTQCEADNLCQGLKICKYGVKFLQIPRATIIIVANISGHLCTAVEFASHADSKRWIK 589
 DB 538 KYVPCGRNLTICGRVCTVTPRKPFHOENGVDVIAFVRDSVCITVDYKLPRTVPDPLAVK 597

QY 590 DGTSCGSKVCRNQRQVSSSLV---GYDCTTDKNDRCVGNKVKHCHSASLYLPDPCSVQ 646
 DB 598 NGSQCDTGRVCRNCRVSRRIKASAVC-SQQCSGHVGVCDNRKNCCHSPGKPFNCQIR 656

QY 647 SLDLPGGSI-----DSGNFPFVPAIPARLPERRYIENIYHSPMRW--PFFLPFIPFFIIFCV 700

Db 657 S---KGFSIFPEDMGSI-----MERASGKTENTWLGFLIPLIV--- 696
 QY 701 LTAIVKVNFORKKWRTEDYSSDEQPESESEPKG 734
 Db 697 -TTAIVLARKQDKWFAKE---EEFSSSEKSEG 726

RESULT 15
 ABJ72102
 ID ABJ72102 standard; protein; 787 AA.
 XX AC ABJ72102;
 XX DT 16-OCT-2003 (first entry)
 XX DE Human membrane bound receptor/protein PRO211340 amino acid sequence.
 XX KW Human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neuroepithelial; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX OS Homo sapiens.
 XX PN US2003065147-A1.
 XX PD 03-APR-2003.
 XX PF 29-AUG-2002; 2002US-00232224.
 XX PR 28-JUL-1999; 99US-0146222P.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2003-522018/49.
 DR N-PSDB; ABT43926.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for the manufacture of a medicament for diagnosing or treating
 PT tumor.
 XX Claim 11; Fig 90; 315pp; English.

This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuroepithelial and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino

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OM protein - protein search, using sw model

Run on: January 10, 2005, 22:07:16 ; Search time 43 Seconds
(without alignments)
1642.398 Million cell updates/sec

Title: US-10-054-683-19
Perfect score: 3984
Sequence: 1 MWVFLSLGLGLRMDSNFD.....WRTDYSSDQPSSEPKG 734
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3984	100.0	734	2 JC4861	fertilin beta cha
2	3687.5	92.6	735	2 G02937	fertilin beta - cr
3	1383.5	34.7	756	2 S47656	tMDC II protein -
4	1365.5	34.3	736	2 S47645	tMDC I protein - C
5	1292	32.4	823	2 S18968	cyrtestin precurs
6	1288	32.3	777	2 I48100	ADAM 5 protein pre
7	1166	29.3	357	2 S23403	sperm surface prot
8	1097	27.5	655	2 JC7850	disintegrin and me
9	1031.5	25.9	825	2 S55060	fertilin alpha-II
10	1022.5	25.7	905	2 S55059	fertilin alpha-I -
11	1016.5	25.5	660	2 S71949	metalloproteinase
12	857	21.5	903	2 S60257	metlin alpha - mo
13	795	20.0	600	2 I49281	fertilin alpha pre
14	766	19.2	826	2 A60385	monocyte surface a
15	762	19.1	609	2 S55270	catrocollastatin p
16	729	18.3	617	2 S48160	metalloproteinase
17	724.5	18.2	732	2 I52361	testicular metallo
18	721	18.1	814	2 G02930	disintegrin-like m
19	719.5	18.1	571	2 S24789	jararagin C precu
20	711	17.8	735	2 I48101	ADAM 6 protein pre
21	710.5	17.8	616	2 A55796	ecarin precursor -
22	698	17.5	776	2 S28258	androgen-regulated
23	696.5	17.5	789	2 S28259	androgen-regulated
24	695	17.4	670	2 I65967	disintegrin-like m
25	692.5	17.4	713	2 I65253	disintegrin-like t
26	663	16.6	610	2 JC7530	vascular apoptosis
27	653.5	16.4	610	2 JC8056	halyase - Gloydiu
28	641	16.1	952	2 T18900	disintegrin and me
29	616.5	15.5	429	2 A42972	coagulation factor

RESULT 1
JC4861
fertilin beta chain - human
C/Species: Homo sapiens (man)
C/Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C/Accession: JC4861
R/Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A/Title: Molecular cloning of the human fertilin beta subunit.
A/Reference number: JC4861; MUID:96295488; PMID:8702389
A/Accession: JC4861
A/Molecule type: mRNA
A/Residues: 1-734 <GUP>
A/Cross-references: UNIPROT:Q99965; GB:U38805; NID:G4151118; PIDN:AAD04206.1; PID:G41511.1
C/Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C/Superfamily: mouse meltrin alpha; disintegrin homology
C/Keywords: Glycoprotein; integrin binding; transmembrane protein
F/382-734/Product: fertilin beta chain #status predicted <NAT>
F/382-467/Domain: disintegrin homology <DIS>
F/448-450/Region: integrin binding #status predicted
F/686-708/Domain: transmembrane #status predicted <TM>
F/121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted

ALIGNMENTS

Query Match	100.0%;	Score 3984;	DB 2;	Length 734;
Best Local Similarity	100.0%;	Pred. No. 5.3e-265;		
Matches	734;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Qy	1	MWVFLSLGLGLRMDSNFDSLPVQITVPEKIRSIIEGIESQASYKIVIEGKPYTNLM	60	
Db	1	MWVFLSLGLGLRMDSNFDSLPVQITVPEKIRSIIEGIESQASYKIVIEGKPYTNLM	60	
Qy	61	QKVFPHNFVYSGTGIMKPLDDQFQNECHQYIEGYPKSVVMVSTCTGLRGVLQFE	120	
Db	61	QKVFPHNFVYSGTGIMKPLDDQFQNECHQYIEGYPKSVVMVSTCTGLRGVLQFE	120	
Qy	121	NVSGIEPLESSVGFEHVIYQVKHKADVSLYNEKDIIESRDLSPKLOSAEPQDFAKYIE	180	
Db	121	NVSGIEPLESSVGFEHVIYQVKHKADVSLYNEKDIIESRDLSPKLOSAEPQDFAKYIE	180	
Qy	181	MHVIVEKQLNHNMGSDTTVAQVQFQIGLTNAIFVSNFTIILSSLELWIDENKIATTG	240	
Db	181	MHVIVEKQLNHNMGSDTTVAQVQFQIGLTNAIFVSNFTIILSSLELWIDENKIATTG	240	
Qy	241	EANELHFTLRWTKSYLVLRPHDVAFLLVYREKSNYVGATFOGKMCDAVAGGVVLHPT	300	
Db	241	EANELHFTLRWTKSYLVLRPHDVAFLLVYREKSNYVGATFOGKMCDAVAGGVVLHPT	300	
Qy	301	ISLESVAVILAQLLSLSMGITTDINKCQCSGAVCIWNPAINPFIHPSGVKIFSNCSFEDEFAH	360	
Db	301	ISLESVAVILAQLLSLSMGITTDINKCQCSGAVCIWNPAINPFIHPSGVKIFSNCSFEDEFAH	360	
Qy	361	FISKQKSCQLHNPRLDPFFKQAVCGNAKLEAGECDGTEQDCALIGETCCDIATCRF	420	

Db 361 FISKQKSOCLHNQPRLDPPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
Qy 421 KAGSNCAEGCCENCLFMSKERMCRPSFECEDLPYCNCGSSASCENHYVQTGHPGCLNQ 480
Db 421 KAGSNCAEGCCENCLFMSKERMCRPSFECEDLPYCNCGSSASCENHYVQTGHPGCLNQ 480
Qy 481 WICIDGVCMSGDQKCTDTFGKEVEFGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDQKCTDTFGKEVEFGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLICKYVGFLLQIPRATIIYANISGHLCAVEFASDHADSQKMWIKDGTSCGNKVC 600
Db 541 CGKLICKYVGFLLQIPRATIIYANISGHLCAVEFASDHADSQKMWIKDGTSCGNKVC 600
Qy 601 RNQRCVSSSYLGVDCTTDCNDRGVNNKXKHCASYLPPDCSVQSDLPFGSIDSNGF 660
Db 601 RNQRCVSSSYLGVDCTTDCNDRGVNNKXKHCASYLPPDCSVQSDLPFGSIDSNGF 660
Qy 661 PPVAIPARLPERRYIENIYHSPKMRWPFLLPFPFIIFCVLIAMVKNFQKWKRTEDY 720
Db 661 PPVAIPARLPERRYIENIYHSPKMRWPFLLPFPFIIFCVLIAMVKNFQKWKRTEDY 720
Qy 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734

RESULT 2
G02937
fertilin beta - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
R;Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A/Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A/Reference number: S55059; MUID:95260313; PMID:7741716
A/Accession: G02937
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-735 <RAM>
A/Cross-references: UNIPROT:Q28478; EMBL:U03959; NID:G998339; PID:G998340
R;Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A/Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A/Reference number: S55059; MUID:95260313; PMID:7741716
A/Accession: G02937
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-722, 'S', 724-735 <PER>
A/Cross-references: EMBL:X77653; NID:G794076; PIDN:CAA54733.1; PID:G794077
C/Superfamily: mouse meltrin alpha; disintegrin homology
F;383-468/Domain: disintegrin homology <DIS>

Query Match 92.6%; Score 3687.5; DB 2; Length 735;
Best Local Similarity 91.3%; Pred. No. 1.1e-244;
Matches 671; Conservative 31; Mismatches 32; Indels 1; Gaps 1;

Qy 1 MW-VLFLSLGGLRMDNSFSLPVQITVPKIRSIKEGIESQASQKIVIEGKPYTNLMQ 59
Db 1 MWRVFLSLGGLRMDNSFSLPVQITVPKIRSIKEGIESQASQKIVIEGKPYTNLMQ 60
Qy 60 MOKNPLPHNFRVYSYSGTGIMKPLDQDFQNFCHQVIEGPKSVVMVSTCTGLRGVLQF 119
Db 60 MOKNPLPHNFRVYSYSGTGIMKPLDQDFQNFCHQVIEGPKSVVMVSTCTGLRGVLQF 120
Qy 120 ENVSGIEPLESSVGFHEVYIVQVKKADVSLYNEKDIERSDLSPKLSAEPQDFPKYI 179
Db 120 ENVSGIEPLESSVGFHEVYIVQVKKADVSLYNEKDIERSDLSPKLSAEPQDFPKYI 180
Qy 180 EMHVIVEKQLYNHMGSDTTVAQKVPQLIGLTNAIFVSNITILSLLELWIDENKIATT 239
Db 180 EMHVIVEKQLYNHMGSDTTVAQKVPQLIGLTNAIFVSNITILSLLELWIDENKIATT 240

Qy 240 GBANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGKMKCDANYAGGVVLHPR 299
Db 241 GDAKELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGKMKCDANYAGGVVLHPR 300
Qy 300 TISLESIAVILAQLLSLSMGIYDDINKQCQSGAVCIMNPEAIHFSGVKIFSNCSFEDA 359
Db 301 TISLESIAVILAQLLSLSMGIYDDINKQCQSGAVCIMNPEAIHFSGVKIFSNCSFEDA 360
Qy 360 HFTSKOKSOCLHNQPRLDPPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCR 419
Db 361 HFTSKOKSOCLHNQPRLDPPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCR 420
Qy 420 FRAGSNCAEGCCENCLFMSKERMCRPSFECEDLPYCNCGSSASCENHYVQTGHPGCLN 479
Db 421 FRAGSNCAEGCCENCLFMSKERMCRPSFECEDLPYCNCGSSASCENHYVQTGHPGCLN 480
Qy 480 QMTICIDGVCMSGDQKCTDTFGKEVEFGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNL 539
Db 481 QMTICIDGVCMSGDQKCTDTFGKEVEFGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNL 540
Qy 540 QCGKLICKYVGFLLQIPRATIIYANISGHLCAVEFASDHADSQKMWIKDGTSCGNKVC 599
Db 541 QCGKLICKYVGFLLQIPRATIIYANISGHLCAVEFASDHADSQKMWIKDGTSCGNKVC 600
Qy 600 CRNRCVSSSYLGVDCTTDCNDRGVNNKXKHCASYLPPDCSVQSDLPFGSIDSNG 659
Db 601 CRNRCVSSSYLGVDCTTDCNDRGVNNKXKHCASYLPPDCSVQSDLPFGSIDSNG 660
Qy 660 FPPVAIPARLPERRYIENIYHSPKMRWPFLLPFPFIIFCVLIAMVKNFQKWKRTED 719
Db 661 FPPVAIPARLPERRYIENIYHSPKMRWPFLLPFPFIIFCVLIAMVKNFQKWKRTED 720
Qy 720 YSSDEQPESESEPKG 734
Db 721 YSTDEQPESESEPKG 735

RESULT 3
S47656
tMDC II protein - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S47656
R;Perry, A.C.F.; Barker, H.L.; Jones, R.; Hall, L.
Biochim. Biophys. Acta 1207, 134-137, 1994
A/Title: Genetic evidence for an additional member of the metalloproteinase-like, disint
A/Reference number: S47656; MUID:94318684; PMID:8043604
A/Accession: S47656
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-756 <PER>
A/Cross-references: UNIPROT:Q28483; EMBL:X77619; NID:G531477; PIDN:CAA54713.1; PID:G53147
C/Superfamily: mouse meltrin alpha; disintegrin homology
F;388-473/Domain: disintegrin homology <DIS>

Query Match 34.7%; Score 1383.5; DB 2; Length 756;
Best Local Similarity 38.1%; Pred. No. 6.6e-87;
Matches 293; Conservative 122; Mismatches 290; Indels 65; Gaps 18;

Qy 3 VLFLSLGGLRMDNSFSLPVQITVPKIRSIKEGIESQASQKIVIEGKPYTNLMQ 61
Db 4 LLVLLTGLGMHADLNPHTFTQTIPEKISSDAKTDPEHNHYVYMITIEGKPYFVHLKK 63
Qy 62 KNFLPHNFRVYSYSGTGI--MKPLDQDFQNFCHQVIEGPKSVVMVSTCTGLRGVLQF 119
Db 64 QSLTSSASFTHSDKMDIRHSPF--LVQMDCNVNGYVAGIPNSLVTLVSLGSLGTQML 121
Qy 120 ENVSGIEPLESSVGFHEVYIVQVKKADVSLYNEKDIERSDLSPKLSAEPQDFPK-- 177
Db 122 KNTSYGLEPNEAVSGFTHKIYEKFDATNILLENDYSWFNSEYQVRKSKSETDFTKLF 181
Qy 178 --YIEMHVIVEKQLYNHMGSDTTVAQKVPQLIGLTNAIFVSNITILSLLELWIDENK 235

```
Db 182 PRYEMHIVVDKLFDFYMGSDINAVTKVQIIGLVNTMLTQLQTLTVIISIEIWSNKNK 241
Qy 236 IATTGEANELHHTFLRWKTSYLVLRPHDVAFLVYREKSNVVGATFOGKMCNDANYAGGV 295
Db 242 ISTTGHAHYVLLFEFFWKDHLNFKPHQIAYLFVYKLPILGATFGQVGNCKDFAAVA 301
Qy 296 LHPRTTISLESIAVLAQLLSMGITVDDINKCOCGAVCIMPEATHFGVGIKFSNCSF 355
Db 302 LYPEGLSLESYTVIIVQLGLNLGLTYDKTDTCSCGDVCTMTPKAVSYSGVGVSVCSL 361
Qy 356 EDPAHFTSKQSCQLNQRLDPFPKQAVCGNAKLEAGBECDCGTQDCCALGETCCDI 415
Db 362 DDFKYISSHNGLTCLQTNPLEMPTYTORRICGNGLLEGGECCGCKNDCT--HKLCCDA 419
Qy 416 ATCRFKAGSCAEGPCC-ENCLFMSKERMCRPSPE-ECDLPEYCNCGSSASCENHYVQTG 473
Db 420 LTCGLKDAQGGSDCCSKCKFKPANTI CRKSDVDECDTFECNGSGYPCLLDITYVRDG 479
Qy 474 HPGCLNQWICIDGCMGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCIGSDSGYTQ 533
Db 480 EYCDSGGAFQGRCTFTDQCDLIGKSGGAPFCFYDEINTRGDKFGNCGTE-----Y 534
Qy 534 CEADNLCQGLICKYVCKFLQIPRATIIYANISGHLICIAVEPASDHA-----581
Db 535 CLFQHLICGLKLVCTWEHKDLISRPNLSVIYAHVRDQTCVSTYLPSPKPPVASTVSKTSY 594
Qy 582 ----DSQKMWIKDGTSCGSKNVCNRQCVSSSYLYGDTT----DKNDRGVCNKKKHCH 633
Db 595 YSVDDRDET FVQDGVCGPDMYCFKMKCKHVFU-MDFETCEASIEGSHGICNNFNHCH 653
Qy 634 CSASYLPDCSVOSDLWPGSDISGNPPVPAIPARLPERRYENIYHSKPMRPPFFLIP 693
Db 654 CEGYNPPHCKPKEAF--GSTDDGLVPA-----EKSYMEGRHAPQKQRFQLI--702
Qy 694 FFIIFCVLI---AIMVKVNFQKKWR-----TEDYSSDEQPESESEPK 733
Db 703 FYISLPVLIITAILIK---RKKLRELCYRGETESESSVSQ-ESSNSK 747

RESULT 4
S47645
tMDC I protein - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47645
R;Barker, H.L.; Perry, A.C.F.; Jones, R.; Hall, L.
Biochim. Biophys. Acta 1216, 429-431, 1994
A;Title: Sequence and expression of a monkey testicular transcript encoding tMDC I, a nd
A;Reference number: S47645; MUID:94325353; PMID:8049267
A;Accession: S47645
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-736 <BAR>
A;Cross-references: UNIPROT:Q28482; EMBL:X76637; NID:9535016; PIDN:CAA54085.1; PID:95350
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;392-477/Domain: disintegrin homology <DIS>

Query Match 34.3%; Score 1365.5; DB 2; Length 736;
Best Local Similarity 36.7%; Pred. No. 1.1e-85;
Matches 281; Conservative 145; Mismatches 270; Indels 69; Gaps 19;

Qy 3 VFLLSGLGLRMDNSFDSLPV-QITVPEKIRSIKEG--IESQASYKIVIEGKPYTVNL 59
Db 4 LLAILSLGLRLTAGPHSETPVQLQITVPRIQNTWNGDVSETHATYSIKIEGKPYTVLL 63
Qy 60 MQKNFLPHNFRVSYSGTGIMKPLDQDF-QNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQ 118
Db 64 EKQSFLPHFLVLYLXNESGLY-VDSFSKGCHCFYQGVADIPKSAVTLATCSGLRGLLQ 122
Qy 119 FENVSYGIEPLESSVGFHYIYQVKH-----KKADVSLYNEK-----DIERSD 161
Db 123 LDNISYGIEPLESSPTVHYVYIKNDIGAIGHFSFQENYPVAQIDYSRILVKVDSNSGA 182
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Qy 162 LSFKLOSAEPQDPAKYIEMHVIIVEKOLYNHMGSDTTTVAQKVFQLIGLTNAIFVSPNIT 221
Db 183 MLSC-----RTLKIIMDKAMDYMGSAVAVAEKVFQIFGLINTMFSQLNIT 231
Qy 222 IILSSLELWTDENKIATTGEANELHHTFLRWKTSYLVLRPHDVAFLVYREKSNVVGATP 281
Db 232 VMLSSLEIWDQNKISTSGHADILQRLFLWKQKLLFQRSHDMTYLLIYRNHSTYVGATY 291
Qy 282 QGKMCNDANYAGGVVLPRTTISLESIAVLAQLLSMGITVDDINKCOCGAVCIMPEA 341
Db 292 HGWACDPKATGALVPKKITVEAFSVMAQLGLNLGLTYDDIYNICYCGPTCIMNPDA 351
Qy 342 IHFGSVKIFSCNCFEDFAHFISKQSQCLNQRLDPFPKQAVCGNAKLEAGBECDCGT 401
Db 352 IRSHGMKFFSCSMDEFFKQIVLPQELKCFQDKTISEMTYQKSAATCGNGILEPTQCCDGY 411
Qy 402 EQCALIGETCCDIATCRFKAGSCAEGPCCEN--CLFMSKERMCRPSFECDLPEYCNCG 459
Db 412 RKACTP--KKCCNPADCTLIGFAECGSGPCCNKTKCTIYARGHVCRKSIDMCDPFYCNCG 469
Qy 460 SSASCENHYVQTGHPGCLNQWICIDGCMGDKQCTDTFGKEVEFGPSECYSHLNSKTD 519
Db 470 TSEFCVPDVAADLEYCSNKTSCYCFKICRDRDRQCSQLFGKFSKANILCTEVEFNQND 529
Qy 520 VSGNCGISDSGYTQCEADNLQCGKLCICKYVCKFLQIPRATIIYANISGHLICIAVEPASD 579
Db 530 KFGNCG-----QRCPPFDILCGKIVCHWITSELPVMTDLDIQTYLGGHVCLSAH-ARN 582
Qy 580 HADSQKMWIKDGTSCGSKNVCNRQCVSSSYLYGDTTDCNDRGVCNKKKHCHCSASYL 639
Db 583 ASKQLGTYTDEDIYACGQKQVCRSGRCRYLSLNITKCTTNCGQNGICNDRFHCQCDPGYA 642
Qy 640 PPDC--SVQSDLPWPGSDISGNPPV--AIPARLPERRYENIYHSKPMRPPFFLIPFF 695
Db 643 PPDCDFSMSS---PGGSDIGFWLSVDKSVPL-FPKQRAAPK---NGLLISFIYFSPLL 695
Qy 696 IIFCVLIAMVKVNFQKKWR-----TEDYSSDEQPESESES 730
Db 696 ILTIAI---VSLKWKMKRFWSKVGTVSSRSRISSED-SSSNNSQSQS 736

RESULT 5
S18968
cyttestin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: I48784; S18968
R;Senftleben, A.; Wallat, S.; Lemaire, L.; Heinlein, U.A.O.
Dev. Growth Differ. 36, 49-58, 1994
A;Title: Pre and postmeiotic germ cell specific expression of Taz83, a gene encoding a p
A;Reference number: I48784
A;Accession: I48784
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-823 <RES>
A;Cross-references: UNIPROT:Q62287; EMBL:X64227; NID:954364; PID:954265
C;Genetics:
A;Gene: Taz83
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;395-480/Domain: disintegrin homology <DIS>

Query Match 32.4%; Score 1292; DB 2; Length 823;
Best Local Similarity 34.2%; Pred. No. 1.4e-80;
Matches 256; Conservative 156; Mismatches 303; Indels 34; Gaps 15;

Qy 4 LFL-LSGLGG-LRMDNSFDSLPVQITVPEKIRSIKEG--IESQASYKIVIEGKPYTVNL 59
Db 5 LFLVLSYLGQVIAAGKDVETPLQITVPEKIDTNIQDAKEATQVTVVTVIEGKAYTLQL 64
Qy 60 MQKNFLPHNFRVSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQ 119
Db 65 EKQSFLPHFLPGTYLRDKLGLTQYFSLVKTHCFYQGHAAEIPVSTVLTSCGLRGLLQ 124
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QY 120 ENVSYGIEPLESSVGFHEHVIYQVKKADVS-----LYNEKDIESRDLSEFKLSABPQQ 173
DB 125 ENTITYGIEPLESSATFEHLYEIKNNKIDYSPLENFANSEQESQSVRIYLVKPEKGSNT 184
QY 174 DPAKYIBMHVIVEKQLYNHNGSDTTVVAAQVQFQIGLITNAIFVSNFTIILSSLELWIDE 233
DB 185 LTKRILRIKIIMDKAMPDHMGSEVGATQKVHIFGLINTWFSQKMTVMLSLEIWESEQ 244
QY 234 NKIATTCGEANELHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGGATFOGKWCMDANYAGG 293
DB 245 DKLETNGDADDEVLRQFLWKSKEISQAQDITLYLLYKDPYVYGATYHGACNPNFTAG 304
QY 294 VMLHPRTISLESIAVILAQLLSMGITDINKKCCSGAVCINMPAIIHFSVKPIFSNC 353
DB 305 IALHPKTLAVEGFAIVLSQLLGLAYDDVNCFCFGSTCINMPAIIHFSVKPIFSNC 364
QY 354 SPEDFAHFIKQKSCQCLHNPRLDPFFKQ--AVCGNAKLEAGEECDCGTEQDCALIGET 411
DB 365 SVDEFKQLASQPELDCLRNTSETFVVPQPGSGYCGNHLLEVPQCDCGPPETCT--HKK 422
QY 412 CCDIATCRFKAGSNCAEGPCE--NCLFMSKERMCRPSFECDLPEYCNSSASCENHY 469
DB 423 CCNPKOCTLIDAAQCGTGPCDCKRTCTAERGRCLCRKSKQCCDPFECNGETEGCAPDTK 482
QY 470 VOTGHPGCLNQWICIDGVCMGDKQCTDTFGKEVEFGFS--ECYSHLNSKTDVSGNCGISD 528
DB 483 AADLEPCNNETAYCFGVCRDPDQCTDLFGKYAK--GPNYVCAQEVNLQNDKFCNC--- 537
QY 529 SGYTQCBADNLQCKLICKYVKGKLLQIPRATIIYANISHLCTAVFASHADSQKQWI 588
DB 538 --HGRCNYSALFCGKAVCYWNAFEBVIQTEKYDQVYTLGGQVCVSAHLRSQTGRDITYV 595
QY 589 KQGTSCSNKVCNRQCVSSSYL--GYDC--TTDCNDRGVCKNKKHCHCSASYLPPDCSV 645
DB 596 HDGTVCSSGQVCFRGDCCLRVHLRGTRCEADCKQCGHICNNLNQCQSGFAPPSCDM 655
QY 646 QSDLPWGGSDISGNFPFVAIPARIPERRIENIYHSPMRPFFLPIFPFIIFCVLIAIM 705
DB 656 TPSS--PGSGMDDGFMLPDKSTPLIFKREH--GLKYKKVLLISFFYLLPFLV-----LAFM 708
QY 706 VKVNFQKRWRTEDYSDSEQESSEPKG 734
DB 709 AVKRMIGKRLAKQNIKALEHKEAFNRG 737
RESULT 6
148100
ADAM 5 protein precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48100
R;Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.
Dev. Biol. 169, 378-383, 1995
A;Title: ADAM, a widely distributed and developmentally regulated gene family encoding m
A;Reference number: I48100; MUID:95269891; PMID:7750654
A;Accession: I48100
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-777 <RES>
A;Cross-references: UNIPROT:Q60472; EMBL:U22060; NID:G965005; PIDN:AAA74918.1; PID:G9650
C;Genetics:
A;Gene: ADAM5
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;395-480/Domain: disintegrin homology <DIS>
Query Match 32.3%; Score 1288; DB 2; Length 777;
Best Local Similarity 35.5%; Pred. NO. 2.4e-80;
Matches 272; Conservative 136; Mismatches 304; Indels 54; Gaps 18;
QY 3 VLFILSLGLGLRMSDPSLVQVITVPEKIESI-IKEGIESQASVKYVIEKPYTNLMQ 61
DB 4 VLVLTLGLGLRYAGNNPRKTFVQTTVPERISSVDTRRHLHNVAIYNITLKGKSYVVRLLK 63
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QY 62 KNFLPHNFRVYSYSGTGIMK--PLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF 119
DB 64 ESFLSGSVIYFYDNRGVQSRQPLPEMD--CSYSGVAGFPHSRVVFATCLGLRGVIOF 121
QY 120 ENVSYGIEPLESSVGFHEHVIYQVKKADVS-----LYNEKDIESRDLSEFKLSABPQQDFA--- 176
DB 122 ENVSYAIEPLESLVSGFTMIYEENNDNTHVPLFGKNSYARIHNLESQGRSSVHKTTVSK 181
QY 177 ---KYTEMHIVVEKQLYNHNGSDTTVVAAQVQFQIGLITNAIFVSNFTIILSSLELWIDE 233
DB 182 LSPRYIDMTIVVNNLFDLGSIDIKTVTKIQLVGLVNAFVQLKHLVLISIEIWSRS 241
QY 234 NKIATTCGEANELHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGGATFOGKWCMDANYAGG 293
DB 242 NKVTNRRPDDDLFRFSDMKRKHVSLKSHVAVYLLTFDKYPEISIGATFPENICNEEYASG 301
QY 294 VMLHPRTISLESIAVILAQLLSMGITDINKKCCSGAVCINMPAIIHFSVKPIFSNC 353
DB 302 IATYPAGLSLESPAVIIVQLLSAGVMYDTSQCYCSTDVCTMTQEAFAVPSGLKDFSTC 361
QY 354 SPEDFAHFIKQKSCQCLHNPRLDPFFKQ--OAVCGNAKLEAGEECDCGTEQDCALI 408
DB 362 SMDNFKYFASQYGLTCLRNTSYDMPYIKQFPFRRRI CGNSIREEGECDCGTLRNT-- 419
QY 409 GETCCDIATCRFKAGSNCAEGPCE--NCLFMSKERMCRPSFE--ECDLPEYCNSSASCPE 466
DB 420 HKKCCDPMQCMCKGKAGCGTGPCTVDCQFQKANVLCKRSVDKDCDFDEYCNRSRSGDCVH 479
QY 467 NHYVQTHGPGCLNQWICIDGVCMGDKQCTDTFGKEVEFGFS--ECYSHLNSKTDVSGNCGI 526
DB 480 DTYAQNQHGFCSGAGFCFNGRCRTHDRQCALFGDSDRGAPFACFACFDEVSNGRDVYGN-- 537
QY 527 SDSGYTQCEADNLQCKLICKYVKGKLLQIPRATIIYANISHLCTAV-----EFASDHA 581
DB 538 ---GRHQYIQLHLCGLVCTWPKQLVSRVNLVVYAHVRDDICVATTKTVKLIIRDLS 594
QY 582 -----DSQKMWIKDGTSCSNKVCNRQCVSSSYLGY-DCTTD-KCNDRGVCKNKKH 631
DB 595 LTTVLLPEDRDETFTVEDGTICGPGQCDKWCFCVEQFINNGSCVAETHCQGRGICNNLDN 654
QY 632 CHCSASYLPPDCSVQSDLPWGGSDISGNFPFVAIPARLPE---RVYENIYHSPMRWP 687
DB 655 CHCHGQFVPECAPKKGQF--GSLDGHVLETTTKTGFRKINMRGV--VLSTKRFQLI 710
QY 688 FFLFIPFFIIFCVLIAIMVKVNFQK---KWRTEYSDSEQESSES 730
DB 711 FYIGIPVILLI---VAAILIKQNLGKLCFGEKHEHMSVSEDSGRS 753
RESULT 7
S23403
sperm surface protein PH-30 beta chain precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jun-2000
C;Accession: S23403; S25696
R;Biolob, C.P.; Wolfsberg, T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
Nature 356, 248-252, 1992
A;Title: A potential fusion peptide and an integrin ligand domain in a protein active in
A;Reference number: S23402; MUID:92204234; PMID:1552944
A;Accession: S23403
A;Molecule type: mRNA
A;Residues: 1-357 <BLOI>
A;Cross-references: EMBL:Z11720
A;Accession: S25696
A;Molecule type: protein
A;Residues: 5-8, 'X', 10-32, 67-88, 125-129, 'X', 131-134, 'X', 136-141, 'X', 143, 154, 'X', 156-161, 'X'
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Keywords: Glycoprotein; transmembrane protein
F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F;5-357/Product: sperm surface protein PH-30 beta chain #status experimental <MAT>
F;5-87/Domain: disintegrin homology <DIS>
F;303-323/Domain: transmembrane #status predicted <TM>
```

F;78,186,256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.3%; Score 1166; DB 2; Length 357;
Best Local Similarity 54.0%; Pred. No. 2.1e-72;
Matches 194; Conservative 62; Mismatches 91; Indels 12; Gaps 4;

QY 378 PFFQQAQVGNKLEAGEECDCGTEQDCALLIGETCCDIATCFKAGSNCAEGPCENCLF 437
DB 1 PVYRNPVCGNRRVEQGGDCGQOECC---DTCCDAATCRKSTSRCAQGPCNQCCEP 57

QY 438 MSKMRCPSPPEECDDLPYCNCGSSASCPENHYVQTGHPGCLNQWICIDGVCMGDKOCTD 497
DB 58 KTKGEVCRESTDECDLPYCNCGSSCAQEDLYVINGHRCANEWIWNRCILSKAQCOE 117

QY 498 TFGKEVFGPSECVSHLNSKTDVSGNCGI-SDSGVYTOCEADNLOGKLIKYVGFLLQI 556
DB 118 TFGTEMEMGSDVCFEQLNTKNDITGNCILSPGNVYKACGASNWKCGKLCISYKSEILRN 177

QY 557 PRATIIYANISGHLCIAVEFASDHADSOQMWIKDGTSCGSKNVCNRCQCVSSYLGYDCT 616
DB 178 KEGMTIYANISGHLCIAVEFASDHADSOQMWIKDGTSCGSKNVCNRCQCVSSYLGYDCT 237

QY 617 TDKNCRGVGNKXKHCASLYPPDCSVQSDLPWGGSIDSGN--FPPVAIPARLPERRY 674
DB 238 PATCSDHGVGNKXKHCCHNPTVPPNCETQSTTFPGSGVSDSGNRYEPI-----PETYF 291

QY 675 IENYHSKPMRWPFFLPIFFPIIFCVLIAIMVKNFQKKWRTEDYSDEQSESEBPX 733
DB 292 VEGAYHTKSRKWPFFLIIPFVIFSVLVATVYVYQKKWKTEDYANDENIESEBPX 350

RESULT 8
JC7850
disintegrin and metalloproteinase (ADAM) 9 protein, short form - human
N;Alternate names: MDC9 protein; meltrin gamma
C;Species: Homo sapiens (man)
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 09-Jul-2004
C;Accession: JC7850
R;Hotoda, N.; Koike, H.; Saegawa, N.; Ishiura, S.
Biochem. Biophys. Res. Commun. 293, 800-805, 2002
A;Title: A secreted form of human ADAM9 has an alpha-secretase activity for APP.
A;Reference number: JC7850; MUID:22050095; PMID:12054541
A;Accession: JC7850
A;Molecule type: mRNA
A;Residues: 1-655 <HOT>
A;Cross-references: UNIPROT:Q8NFM6; GB:AF495383
A;Comment: This protein, which is a member of the a disintegrin and metalloprotease (ADAM) family, is proteolytically active, and has an alpha-secretase activity for a number of substrates.
C;Genetics:
A;Gene: adam9

Query Match 27.5%; Score 1097; DB 2; Length 655;
Best Local Similarity 36.5%; Pred. No. 2.3e-67;
Matches 241; Conservative 120; Mismatches 241; Indels 58; Gaps 20;

QY 2 WVLFL-LSG---LG---GLRMSNFDLPVQITVPEKIRSIIRKGG---IESQASYKIVIE 51
DB 16 WLLLLGLVGPVLAARPGFQQTSHLS--YEIITPWLTRERREAPRPSYKQSVYVLAQ 73

QY 52 GKPTVNL-MQKNFLPNFRVYSYSGIMKPLDQDFQNFCHYGYIEGPKSVVMVYSTC 110
DB 74 GKEHIIHLERNKOLLPPDFVYTYNKEGTLITDPNIQNHCHYGYVGVHNSIALSDC 133

QY 111 TGLRGVLQFENVSYGIEPLESSVGFHVIVQV-----KHKKADVSLYNEKDIESR----- 160
DB 134 FLGLGLHLENASVGIPLQNSHFEHIIYRMDVYKEPLKCGVS---NKDIEKETAKDE 190

QY 161 -----DLSFKLQSAEPQDFAKYEIMHVIVEKQLYNHMGSDTTVVAQKVFLIGLTN 212
DB 191 EEEPPSTQLLRRAVLQ---TRYVELFIVVDKERYDMGRNQTAVEREMILLANYLD 247

QY 213 AIFVSNITILSLELWIDENKIATTGEANELLHTFLRWKTSYLV-LRPHDVAFLVYR 271
DB 213 AIFVSNITILSLELWIDENKIATTGEANELLHTFLRWKTSYLV-LRPHDVAFLVYR 271

DB 248 SMYIMLIRIVLVGLEIWTNGNLINIVGGAGDVLGNGFVQWREKFLITRRRHDSALVLKK 307

QY 272 EKSNYVGATFQGMCDANYAGGVVLHPRITISLESLAVILAQLLSLMGITYDDINKCQCS 331
DB 308 GFGGTAGWAFVGTVCSSHAGGINVFGQ-ITVETFAFASIVAHGHLGNLGMNHHDDGRDCSCG 366

QY 332 GAVCIMNPEAIHFGSVKIFSNCSFEDFAHFISKQSOCLHNQPLDLPFFKQOAVCGNAKL 391
DB 367 AKSCIMNSGA---SGSRNFSCSAEDFEKLTNLKGGNCLLNIPKPDEAYSAPS-CGNKLV 422

QY 392 EAGSECCGTBODCALLIGETCCDIATCFKAGSNCAEGPCENCLFMSKMRCPSPREC 451
DB 423 DAGSECCGTBPKCEL--DPCCEGSTCKLKSFAACAYGDCDCRFLPGGTLCRGKTSCE 480

QY 452 DLPEYCNCGSSASCPENHYVQTGHPGCLNQWICIDGVCMGDKQCTDTDFGKEVEFGPSECY 511
DB 481 DVPEYCNCGSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYDYDAQCOVIFGSKAKAAPKDCF 540

QY 512 SHLNSKTDVSGNCGISDSGYTQCEADNLOGKLIKYVGFLLQIPRATIIYANIS----- 567
DB 541 IEVNSKGRDFGNGCFGSGNEYKCKATGNALCGKQACENV---QBIPVFGIVPAIIQTSPR 596

QY 568 GHLCLIAVEF--ASDHADSQMWIKDGTSCGSKNVCNRCQCVSSYLGYDCTD-KCNDRG 624
DB 597 GTKCGVDVQLGSDVDPDG--MVNEGTKCGAGKICRNPQCVDASVLNVDVQKKCHGHG 654

RESULT 9
S55060
fertilin alpha-II - crab-eating macaque
C;Species: Macaca fascicularis (Crab-eating macaque)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S55060
R;Perly, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A;Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A;Reference number: S55059; MUID:95260313; PMID:7741716
A;Accession: S55060
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-825 <PER>
A;Cross-references: UNIPROT:Q28477; EMBL:X79809; NID:G794074; PIDN:CAA56204.1; PID:G79404
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;443-523/Domain: disintegrin homology <DIS>
F;377/Active site: Glu #status predicted

Query Match 25.9%; Score 1031.5; DB 2; Length 825;
Best Local Similarity 33.6%; Pred. No. 9.4e-63;
Matches 252; Conservative 117; Mismatches 307; Indels 75; Gaps 28;

QY 25 QITVPEKIRSIIRKIEGIESQASYKIVIEGKPYTNL-MQKNFLPNFRVYSYSGTGMKPL 83
DB 81 EIVIPKELMVRGSEDSVEKATYLLMQGQHLVHLKVRSHFVNFPVYSYH-NGILQOE 139

QY 84 DQDFQNFCHYGYIEGPKSVVMVYSTCTGLRGVLQFENVSYGIEPLESSVGFHVIVQVK 143
DB 140 SPFIHSDCHYGYIEGPKSVFVSNTCAGLGLILKEEKSVSIEPMDSSRRFEHLVTMA 199

QY 144 HKKADVSLYNEKDIESRD-----LSFKLQSAEPQO-----DFAKYIEMHVIVEKQLY 190
DB 200 H-EARVSC-----GVTSRDSHVSTSWQGSRKPHDLQALSYLEMSHTKYEMFVVVNNQRF 254

QY 191 NHMGSDTTVVAQKVFLIGLTNAIFVSFNITILSLELWIDENKIATTGEANELLHTFL 250
DB 255 QMGNSINETVQRVVDVIALANGFTRGINTVEVLAGEIWTGDLIDVAVDLQITLRFN 314

QY 251 RWKTSYLVLR-PHDVAFLVYREKSNYVGATFGKMDANYAGGV-VLHPRITISLES LAV 308
DB 315 RWRQMLFRRAKHDAVHIVGHHPGQNTGQAFLSGACSSGFAAAVESFHEDMLL--FAA 372

QY 309 ILAQLLSLMGITYDDINKCQ--SGAVCIWNPAIHGSKVIFSNCSFEDFAHFISKQKS 367
DB 373 LMVHGLHNLGIQHDH-SACFCREKHPCLMHENITKESG---FSNCSSDYVPHQLRHHKG 428

```
QY 368 QCLHNPRLDPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCA 427
D 369 FAALVWHELHGLGIQHDH-SACFCKEKFCLMHNITKESG---FSCNCSDFHOFLE 424
QY 365 QKSOCLHNPRLDPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGS 424
D 425 HKGACLFNPRGRKRRDSACGNGVDETECCGSA--CHL--DPCCD-PTCTLKEHA 479
QY 425 NCAEGPCCNCLPMSKERMCRPSFECEDLPYCNCGSSASCPENHYVQTGHPGCLNQCWICI 484
D 480 ECHGLCLDCTFRKGFCLCRPTQDECDLPYCGSSAECPADSKQDGTGLCDRIHY-CS 538
QY 485 DGVCMGDKQCTDTFGKEVEFGSECYSHLNSKTDVSGNCG---ISDSGYTQCEADNLCQ 541
D 539 GGCKNPDNQCVMNIYGPARSAPEDCYISNTRGDRFGNCGHPTEDQOYTVTSCDDNVFC 598
QY 542 GKLIKVVGKFLQIPRA---TIIYANISGHLCIAVEF--ASDHADSOQRMWKDGTSCG 595
D 599 GKLICITGV---QSLPRVKAQHTVIQVPHDNDWCMSMDADNITDTPDNGNVHV--GTSCA 652
QY 596 SNKVCNRQCVSSYLYGDTCTDK-CNDRGVGNKKHCHCSASYLPPDCSVQSDLPWPGGS 654
D 653 PNKVCCTDYSVHSHILLYDCRPEESCHGKGVNLRHCHCESGFAPDCKNPGN---GGS 709
QY 655 IDSGNFPFVAIPARLPERRYENIYHSPMRP-----PFLFPIFFIICVLIAMVKVN 709
D 710 VDSG---PFGMQVTNNSGSESIARGQSLRQDQVYKLVLLVPLFLV--LLLCSLLTIS 764
QY 710 FORKKWRT-----EDYSSDEQPESE 729
D 765 YLCSEVQTAVAEVESSTETLESE 789

RESULT 10
S55059
fertilin alpha-I - crab-eating macaque
C/Species: Macaca fascicularis (Crab-eating macaque)
C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: S55059
R/Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A/Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A/Reference number: S55059; MUID:95260313; PMID:7741716
A/Accession: S55059
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-905 <PR>
A/Cross-references: UNIPROT:Q28476; EMBL:X79808; NID:G794072; PIDN:CAAS6203.1; PID:G7940
C/Superfamily: mouse meltrin alpha; disintegrin homology
F/442-522/Domain: disintegrin homology <DIS>
F/376/Active site: Glu #status predicted

Query Match 25.7%; Score 1022.5; DB 2; Length 905;
Best Local Similarity 33.6%; Pred. No. 4.4e-62;
Matches 250; Conservative 123; Mismatches 297; Indels 75; Gaps 29;

QY 22 LPQVITVPEKRSIIKIGIESQASKIVIEGKPYTNL-WQKNFLPHNFRVYSYSGTGIM 80
D 83 IKPLTVOGGDSSV--EGL-----SYLLFMQKQHLVHKVRSHFVNFPVYSYH-NGIL 135
QY 81 KPLDQDFONFCHYQGYEGPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFHVY 140
D 136 QGSPFPIHSDCHYEGYEGVSGSFVNTNAGLRLGILKEKSYSIIEPMOSSRRFEHVLY 195
QY 141 QVGHKKADVSLYNEKDIETSRD-----LSFKLQSAEPQO-----DPKYEIMHVIIEK 187
D 196 TMAH-EARVSC---GVTSRDSHVSTSWQGRSKPHDLQALS YLWSHTKYEMFVVVNN 250
QY 188 QLYNHMGSDITVAQKVQFOLIGLNTALFVSNITILLSSLELWIDENKIATTEGANELH 247
D 251 QRFQMGNSINETQVRVVDVJALANGFTRGINTVWLAGMEIWTGDLIDVANDLQITLR 310
QY 248 TFLRWKTSYLVLR-PHDVAFLLVYREKSNVYCATFGQKMCNDANYAGV-VLHPRTISLES 305
D 311 NFNEWRQEMLFRRAKHDVAHVHGHFQNTGQAFLSGACSSGFAAAVESFHEDMLL-- 368
```

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QY 306 LAVILAQLLSMGITYDDINKQC--SGAVCMNPNPAIHFSGVKVI FSNCSFEDFAHFISK 364
D 369 FAALVWHELHGLGIQHDH-SACFCKEKFCLMHNITKESG---FSCNCSDFHOFLE 424
QY 365 QKSOCLHNPRLDPFFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGS 424
D 425 HKGACLFNPRGRKRRDSACGNGVDETECCGSA--CHL--DPCCD-PTCTLKEHA 479
QY 425 NCAEGPCCNCLPMSKERMCRPSFECEDLPYCNCGSSASCPENHYVQTGHPGCLNQCWICI 484
D 480 ECHGLCLDCTFRKGFCLCRPTQDECDLPYCGSSAECPADSKQDGTGLCDRIHY-CS 538
QY 485 DGVCMGDKQCTDTFGKEVEFGSECYSHLNSKTDVSGNCG---ISDSGYTQCEADNLCQ 541
D 539 GGCKNPDNQCVMNIYGPARSAPEDCYISNTRGDRFGNCGHPTEDQOYTVTSCDDNVFC 598
QY 542 GKLIKVVGKFLQIPRA---TIIYANISGHLCIAVEF--ASDHADSOQRMWKDGTSCG 595
D 599 GKLICITGV---QSLPRVKAQHTVIQVPHDNDWCMSMDADNITDTPDNGNVHV--GTSCA 652
QY 596 SNKVCNRQCVSSYLYGDTCTDK-CNDRGVGNKKHCHCSASYLPPDCSVQSDLPWPGGS 654
D 653 PNKVCCTDYSVHSHILLYDCRPEESCHGKGVNLRHCHCESGFAPDCKNPGN---GGS 709
QY 655 IDSGNFPFVAIPARLPERRYENIYHSPMRP-----PFLFPIFFIICVLIAMVKVN 709
D 710 VDSG---PFGMQVTNNSGSESIARGQSLRQDQVYKLVLLVPLFLV--LLLCSLLTIS 764
QY 710 FORKKWRT-----EDYSSDEQPESE 729
D 765 YLCSEVQTAVAEVESSTETLESE 789

RESULT 11
S71949
metalloproteinase 12 (EC 3.4.24.-) precursor - human
A/Alternate names: disintegrin 12; myeloma cell metalloproteinase MCMP
C/Species: Homo sapiens (man)
C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C/Accession: S71949; PC4264
R/McKie, N.; Dallas, D.J.; Edwards, T.; Apperley, J.F.; Russell, R.G.G.; Croucher, P.I.
Biochem. J. 318, 459-462, 1996
A/Title: Cloning of a novel membrane-linked metalloproteinase from human myeloma cells.
A/Reference number: S71949; MUID:96404892; PMID:88609033
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-660 <MCK>
A/Cross-references: UNIPROT:Q13443
A/Experimental source: myeloma cells
R/McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,
Biochem. Biophys. Res. Commun. 230, 335-339, 1997
A/Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM)
A/Reference number: PC4263; MUID:97168971; PMID:9016778
A/Accession: PC4264
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-337 <MCF>
A/Experimental source: articular chondrocyte
C/Function:
A/Note: involved in cell/cell and cell/matrix interaction in a variety of cell ty
C/Note: membrane-bound; belongs to repolysin family of metalloproteinases
C/Superfamily: mouse meltrin alpha; disintegrin homology
C/Keywords: hydrolase; metalloproteinase; zinc
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-660/Product: pre-metalloproteinase 12 #status predicted <MAT>
F/54-59/Region: autoinhibitory
F/295-378/Domain: disintegrin homology <DIS>
F/574-598/Region: epidermal growth factor-like
F/622-642/Domain: transmembrane #status predicted <TM1>
F/57,229,233,239/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status i
F/229,233,239/Binding site: zinc, catalytic (His) (active) #status predicted
F/230/Active site: Glu #status predicted
```



```
Db 197 FRFVLELVVDKAMVTNRNGDLDKIKTRMYEIVNTVNEIYRYMYIHVALVGLIWSNEDK 256
Qy 236 IATTGEANEILLHTFLRW-KTSYLVLRPHDVAFLVYREKSNYVGATFQGRKMCDAANYAGGV 294
Db 257 ITVKPEAGYTLNAFGEWRKTDLLTRKKGHNAQLLTAIDLDRVIGLAVVGSMSCHPKRSTGI 316
Qy 295 VLHPRITISLESILAVILAQLLSLMSGITYDDINKQCSGAVCIIMNPEAIHFSGVKIFSNCS 354
Db 317 IODYSEINL-VVAVIMAHMGHNLGINHDS-GYCSCGDYACIMRPE-ISPEPSTFFSNCS 373
Qy 355 PEDPAHFISKQSOCLNQPRLDFFKQQAACGNKLEAGBECDCGTEQDCALIGETCCD 414
Db 374 YFECWDFIMNHNPECILNEP-LGTDIISPVCNGLLEVBECDCGTPENCQ---NECCD 429
Qy 415 IATCRFXAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNNGSSASCENHYVQTGH 474
Db 430 AATCKLKSQCGHGDCEQCKFSKSGTECRASMECDPAEHCTGQSSECPADVPHKNGQ 489
Qy 475 PCGLNQWICIDGVCMGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQC 534
Db 490 PCLDNYGYCNGNCPIMYHQCYDLFGADVYEAEADSCFER-NQKGNYYGYCRKENGKIPC 548
Qy 535 EADNLQCGKLCIKYVGRFLQIPRATIIYANISGHLCIAVEFASDHADSKMWIKDGTSC 594
Db 549 APEDVKCGRLYCK-----DNSPGQNNPCMKMFYSNE-DEHKGWVLPGTTC 591
Qy 595 GSNKVCERNQRCV 606
Db 592 ADGKVCNHCVCV 603
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Search completed: January 10, 2005, 22:28:33
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 22:04:22 ; Search time 201 Seconds
(without alignments)
2101.119 Million cell updates/sec

Title: US-10-054-683-19

Perfect score: 3984

Sequence: 1 MWVFLSLGLGURMSNFD.....WRTEDYSSDEQPSESEPKG 734

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3369.5	99.6	735	1 AD02 HUMAN	Q9965 homo sapien
2	3690.5	92.6	735	1 AD02 MACFA	Q28478 macaca fasc
3	3065.5	76.9	579	2 Q6P2G0	Q6P2G0 homo sapien
4	3065.5	76.9	579	2 AAH64547	AAH64547 homo sapi
5	2820	70.8	735	2 Q866A8	Q866A8 sus scrofa
6	2723	68.3	745	1 AD02 BOVIN	Q77780 bos taurus
7	2685	67.4	751	1 AD02 RABIT	Q28660 oryctolagus
8	2479.5	62.2	737	1 AD02 RAT	Q63202 rattus norv
9	2453.5	61.6	735	1 AD02 MOUSE	Q60718 mus musculu
10	2326	58.4	735	1 AD02 CAVPO	Q60411 cavia porce
11	1586.5	39.8	746	1 AD18 MACFA	Q95134 macaca fasc
12	1582.5	39.7	739	1 AD18 HUMAN	Q9Y3G7 homo sapien
13	1524.5	38.3	787	2 Q8TC27	Q8TC27 homo sapien
14	1524.5	38.3	787	2 AAQ89099	AAQ89099 homo sapi
15	1519.5	38.1	787	2 Q8TC42	Q8TC42 homo sapien
16	1493.5	37.5	715	2 Q6UXJ9	Q6UXJ9 homo sapien
17	1493.5	37.5	715	2 AAQ88687	AAQ88687 homo sapi
18	1437.5	36.1	750	2 Q6P901	Q6P901 mus musculu
19	1437.5	36.1	750	2 AAH60983	AAH60983 mus muscu
20	1433	36.0	750	2 Q8K410	Q8K410 mus musculu
21	1383.5	34.7	756	2 Q28483	Q28483 macaca fasc
22	1371.5	34.4	730	2 Q80Y08	Q80Y08 mus musculu
23	1367.5	34.3	677	2 Q8B080	Q8B080 mus musculu
24	1366.5	34.3	719	1 AD18 MOUSE	Q9r157 mus musculu
25	1365.5	34.3	736	2 Q28482	Q28482 macaca fasc
26	1293	32.5	822	2 Q62287	Q62287 mus musculu
27	1292	32.4	740	2 P70534	P70534 rattus norv
28	1288	32.3	777	2 Q60472	Q60472 cavia porce
29	1237	31.0	771	2 Q8CDV5	Q8CDV5 mus musculu
30	1237	31.0	771	2 Q9DAF0	Q9DAF0 mus musculu
31	1211	30.4	819	1 AD09_HUMAN	Q13443 homo sapien

32	1206	30.3	751	2	Q60816	Q60816 mus musculu
33	1166	29.3	845	1	AD09_MOUSE	Q61072 mus musculu
34	1161.5	29.2	873	2	O42595	O42595 xenopus lae
35	1059	26.6	919	2	Q28659	Q28659 oryctolagus
36	1042	26.2	792	2	O19061	O19061 saquinus oe
37	1041	26.1	812	2	O77779	O77779 bos taurus
38	1031.5	25.9	825	2	Q28477	Q28477 macaca fasc
39	1028.5	25.8	791	1	AD1A_MOUSE	Q60813 mus musculu
40	1024.5	25.7	789	1	AD01_RAT	P70505 rattus norv
41	1022.5	25.7	905	2	Q28476	Q28476 macaca fasc
42	1016	25.5	821	2	O19060	O19060 saquinus oe
43	1015.5	25.5	825	2	O46652	O46652 papio anubi
44	1014.5	25.5	838	2	O19056	O19056 papio anubi
45	1002.5	25.2	804	2	Q60410	Q60410 cavia porce

ALIGNMENTS

RESULT 1
AD02_HUMAN
ID AD02_HUMAN STANDARD; PRT; 735 AA.
AC Q9965: P78326: Q9UQ08;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30).
GN Name=ADAM2; Synonyms=FTNB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=97193554; PubMed=9041139;
RA Vidaeus C.M., von Kap-Herr C., Golden W.L., Eddy R.L., Shows T.B.,
RA Herr J.C.;
RT "Human fertilin beta: identification, characterization, and
RT chromosomal mapping of an ADAM gene family member.";
RL Mol. Reprod. Dev. 46:363-369 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=96295488; PubMed=8702389;
RA Gupta S.K., Alves K., Palladino L.O., Mark G.E., Hollis G.F.;
RT "Molecular cloning of the human fertilin beta subunit.";
RL Biochem. Biophys. Res. Commun. 224:318-326 (1996).
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Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Basa S.S., Loquellano N.A., Peters G.J., Abraham R.D., Mullahy S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Sperm surface membrane protein that may be involved in
CC sperm-egg plasma membrane adhesion and fusion during
CC fertilization. Could have a direct role in sperm-zona binding or
CC migration of sperm from the uterus into the oviduct. Interactions
CC with egg membrane could be mediated via binding between its
CC disintegrin-like domain to one or more integrins receptors on the
CC egg. This is a non catalytic metalloprotease-like protein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC -1- Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q99965-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q99965-2; Sequence=VSP_005471;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expressed specifically in spermatogenic cells
CC in the seminiferous cells. Not detected in fetal tissues.
CC -1- DOMAIN: A tripeptide motif (PEE) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding.
CC -1- PM: The prodomain and the metalloprotease domain are cleaved
CC during the epididymal maturation of the spermatozoa.
CC -1- MISCELLANEOUS: In mammals, exists as a heterodimer composed of an
CC alpha and beta subunits. In human, fertilin alpha is a pseudogene.
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.

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DR EMBL; U52370; AAC51110.1; -;
DR EMBL; U38805; AAD04206.1; -;
DR EMBL; X93974; CAA67753.1; -;
DR EMBL; AJ133005; CAB40813.1; -;
DR EMBL; BC034957; AAH34957.1; -;
DR PIR; JC4861; JC4861.
DR HSP; P30403; IY4Y.
DR MEROPS; M12.950; -;
DR GENE; HGNC:198; ADAM2.
DR MIM; 601533; -;
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005178; F: integrin binding; TAS.
DR GO; GO:0008237; F: metalloprotease activity; TAS.
DR GO; GO:0007342; P: fusion of sperm to egg plasma membrane; TAS.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR002870; Peptidase M12B_N.
DR InterPro; IPR006025; Pept_M12B_BS.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Fep M12B propep; 1.
DR Pfam; PF01421; Reptolysin; 1.

DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE NEG.
DR PROSITE; PS01186; EGF_2; FALSE NEG.
KW Alternative splicing; Cell adhesion; EGF-like domain; Glycoprotein;
KW Signal; Transmembrane.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 174
FT CHAIN 175 735 ADAM 2.
FT DOMAIN 175 686 Extracellular (Potential).
FT TRANSMEM 687 707 Potential.
FT DOMAIN 708 735 Cytoplasmic (Potential).
FT DOMAIN 175 382 Metalloprotease-like.
FT DOMAIN 383 475 Disintegrin-like.
FT DOMAIN 477 606 Cys-rich.
FT DOMAIN 612 645 EGF-like.
FT DISULFID 287 370 By similarity.
FT DISULFID 329 354 By similarity.
FT DISULFID 445 458 Potential.
FT DISULFID 616 627 By similarity.
FT DISULFID 621 633 By similarity.
FT DISULFID 635 644 By similarity.
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 459 459 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 566 566 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 172 190 Missing (in isoform 2).
FT FTId=VSP_005471.
FT CONFLICT 3 3 Missing (in Ref. 2).
FT CONFLICT 21 21 E -> H (in Ref. 3).
FT CONFLICT 99 99 E -> D (in Ref. 3).
FT CONFLICT 106 106 V -> G (in Ref. 3).
FT CONFLICT 170 170 V -> A (in Ref. 2).
FT CONFLICT 288 288 D -> H (in Ref. 1).
FT CONFLICT 321 321 I -> T (in Ref. 1).
FT CONFLICT 388 388 G -> S (in Ref. 3).
FT CONFLICT 396 398 EEC -> DEF (in Ref. 3).
FT CONFLICT 501 501 G -> S (in Ref. 3).
FT CONFLICT 529 529 D -> Y (in Ref. 3).
FT CONFLICT 579 579 S -> G (in Ref. 3).
FT CONFLICT 588 588 M -> L (in Ref. 3).
FT CONFLICT 603 603 NK -> KQ (in Ref. 3).
FT CONFLICT 629 630 NK -> KQ (in Ref. 3).
FT CONFLICT 638 638 S -> F (in Ref. 3).
SQ SEQUENCE 735 AA; 82456 MW; 92867B5340BEE01F CRC64;

Query Match 99.6%; Score 3969.5; DB 1; Length 735;
Best Local Similarity 99.7%; Pred. No. 1.2e-261;
Matches 733; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MW-VLFLSLGLGRMDSNFDLPVQITVPEKIRSIKEGIESQASQYKIVIEGKPYTVNL 59
Db 1 MWRVFLSLGLGRMDSNFDLPVQITVPEKIRSIKEGIESQASQYKIVIEGKPYTVNL 60
Qy 60 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGVLQF 119
Db 61 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGVLQF 120
Qy 120 ENVSYGIEPLESSVGFPHVYQVKKKADVSLNKKDIESRDLSEFKLQSPQDFPKYI 179
Db 121 ENVSYGIEPLESSVGFPHVYQVKKKADVSLNKKDIESRDLSEFKLQSPQDFPKYI 180
Qy 180 EMHVIVEKQLYNHMGSDTTVAQKVFQIGLTLNATFVSFNITILSSLEWIDENKIATT 239
Db 181 EMHVIVEKQLYNHMGSDTTVAQKVFQIGLTLNATFVSFNITILSSLEWIDENKIATT 240
Qy 240 GEANELHTFLRWKTSYLVLRPHDVAFLVYREKSNVYGVATFGQKMCDCANDYAGVVLHPR 299

Db 241 GEANELHTEFLRMKTSYLVLRPHDVAFLVYREKSNVYGFQGMCDANYAGVWLHPR 300
Qy 300 TISLESIAVLAQLLSLSMGTDDINKCQSGAVCIWNPENAIHFGSKVIFNSGSPDFA 359
Db 301 TISLESIAVLAQLLSLSMGTDDINKCQSGAVCIWNPENAIHFGSKVIFNSGSPDFA 360
Qy 360 HFTSKQKSQLHNPRLDPFFKQAVCGNAKLEAGEBCDGTEDCALIGETCCDIATCR 419
Db 361 HFTSKQKSQLHNPRLDPFFKQAVCGNAKLEAGEBCDGTEDCALIGETCCDIATCR 420
Qy 420 FKAGSNCAEGPCPCNCLFMSKRCRPSRECDLPYCNCGSSASCENHYVQTHGPCGLN 479
Db 421 FKAGSNCAEGPCPCNCLFMSKRCRPSRECDLPYCNCGSSASCENHYVQTHGPCGLN 480
Qy 480 QWICIDGVCMSGDKQCTDTFGKEVFGPSECYSHLNSKTDVSGNCGISDSGYTOCEADNL 539
Db 481 QWICIDGVCMSGDKQCTDTFGKEVFGPSECYSHLNSKTDVSGNCGISDSGYTOCEADNL 540
Qy 540 QCGKLIKYVGFLLQIPRATIIYANISGHLCIAVEFASDHADSKQWIKDGTSCGNKV 599
Db 541 QCGKLIKYVGFLLQIPRATIIYANISGHLCIAVEFASDHADSKQWIKDGTSCGNKV 600
Qy 600 CRNORCVSSVLYGVDCTDKNDRGVGNKKGCHCSASYLPDSCVQSDLWPGGSDSGN 659
Db 601 CRNORCVSSVLYGVDCTDKNDRGVGNKKGCHCSASYLPDSCVQSDLWPGGSDSGN 660
Qy 660 FPPVAIPARIPERYIENIYHSHKPMRPFLLFPFFIFCVLIAIMVKNVFORKKWRTED 719
Db 661 FPPVAIPARIPERYIENIYHSHKPMRPFLLFPFFIFCVLIAIMVKNVFORKKWRTED 720
Qy 720 YSSDEQSESESEPKG 734
Db 721 YSSDEQSESESEPKG 735

RESULT 2

ID AD02 MACFA STANDARD; PRT; 735 AA.
AC Q28478; Q28472;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
GN Name=ADAM2; Synonyms=FTNB;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP TISSUE=Testis;
RC MEDLINE=95260313; PubMed=7741716;
RA Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
RT "Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms";
RL Biochem. J. 307:843-850(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=96341733; PubMed=8720115;
RA Ramarao C.S., Myles D.G., White J.M., Primakoff P.;
RT "Initial evaluation of fertilin as an immunoreceptive antigen and molecular cloning of the cynomolgus monkey fertilin beta subunit.";
RL Mol. Reprod. Dev. 43:70-75(1996).
CC -1- FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein (By

similarity).
CC -1- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -1- DOMAIN: A tripeptide motif (FDE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).
CC -1- PTM: The signal and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X77653; CAA54733.1; -.
CC EMBL; U33959; AAB52699.1; -.
CC PIR; G02937; G02937.
CC HSP; P30403; IN4Y.
CC MEROPS; M12.950; -.
CC InterPro; IPR006586; ADAM cysteine.
CC InterPro; IPR001762; Disintegrin.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR001590; Peptidase M12B.
CC InterPro; IPR002870; Peptidase M12B_N.
CC Pfam; PF00200; Disintegrin; 1.
CC Pfam; PF01562; Pep M12B proper; 1.
CC Pfam; PF01421; Reptolysin; 1.
CC PRINTS; PR00289; DISINTEGRIN.
CC ProDom; PD000664; disintegrin; 1.
CC SMART; SM00608; ACR; 1.
CC SMART; SM00050; DISIN; 1.
CC PROSITE; PS00215; ADAM MEPRO; 1.
CC PROSITE; PS00427; DISINTEGRIN_1; 1.
CC PROSITE; PS00214; DISINTEGRIN_2; 1.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS00026; EGF_3; 1.
CC Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 174 By similarity.
FT CHAIN 175 735 ADAM 2.
FT DOMAIN 17 686 Extracellular (Potential).
FT TRANSMEM 687 707 Potential.
FT DOMAIN 708 735 Cytoplasmic (Potential).
FT DOMAIN 175 382 Metalloprotease-like.
FT DOMAIN 383 475 Disintegrin-like.
FT DOMAIN 476 606 Cys-rich.
FT DOMAIN 612 645 EGF-like.
FT DISULFID 287 370 By similarity.
FT DISULFID 329 354 By similarity.
FT DISULFID 445 458 Potential.
FT DISULFID 616 627 By similarity.
FT DISULFID 621 633 By similarity.
FT DISULFID 635 644 By similarity.
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 459 459 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 566 566 N-linked (GlcNAc...) (Potential).
FT CONFLICT 723 723 S -> T (in Ref. 2).
SQ SEQUENCE 735 AA; 82357 MW; BE84BE115E1D0B53 CRC64;
Query Match 92.6%; Score 3690.5; DB 1; Length 735;
Best Local Similarity 91.4%; Pred. No. 1.1e-242;

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Matches 672; Conservative 30; Mismatches 32; Indels 1; Gaps 1;
Qy 1 MW-VLFLSLGLGLRMDNSFSLPQVITVPEKIRSIIEKIEGIESQASYKIVIEGKPYTVNL 59
Db 1 MWRVFLSLGLGLRMDNSFSLPQVITVPEKIRSIIEKIEGIESQASYKIVIEGKPYTVNL 60
Qy 60 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHVQYIEGYPKSVVMVSTCTGLRGVLQF 119
Db 61 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHVQYIEGYPKSVVMVSTCTGLRGVLQF 120
Qy 120 ENVSYGIEPLESSVGFPEHVIYQVKKADVSLYNEKDIESRDLSEKLSQAEPOODFAKYI 179
Db 121 ENVSYGIEPLESSVGFPEHVIYQVKKADVSLYNEKDIESRDLSEKLSQAEPOODFAKYI 180
Qy 180 EMHVIVEKQLYNNHMGSDTTTVAQVFLIGLITNAIFVSNITILSLSELEWIDENKIATT 239
Db 181 EMHVIVEKQLYNNHMGSDTTTVAQVFLIGLITNAIFVSNITILSLSELEWIDENKIATT 240
Qy 240 GEANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYGATFOGKMCNDANYAGGVLLHPR 299
Db 241 GDAKELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYGATFOGKMCNDANYAGGVLLHPR 300
Qy 300 TISLESIAVILAOQLLSLMSGITYDDINKCQCSGAVCIIMNPEAIFHSGVKIFSNCSFEDFA 359
Db 301 TISLESIAVILAOQLLSLMSGITYDDINKCQCSGAVCIIMNPEAIFHSGVKIFSNCSFEDFA 360
Qy 360 HFISKQSKQCLHNPRLDPPFKQAVCGNKLAGEECDCGTEQDCALIGETCCDIATCR 419
Db 361 HFISKQSKQCLHNPRLDPPFKQAVCGNKLAGEECDCGTEQDCALIGETCCDIATCR 420
Qy 420 FKAGSNCAEGPCCNCLFMSKERMCRPSFECDLPYCNCGSSASCENHYVQTGHPCGLN 479
Db 421 FKAGSNCAEGPCCNCLFMSKERMCRPSFECDLPYCNCGSSASCENHYVQTGHPCGLN 480
Qy 480 QWICIDGVCMNGDKQCDMTDFGEAEFGTECYSLNKTVDVSGNCGISDGYTTOCEADNL 539
Db 481 QWICIDGVCMNGDKQCDMTDFGEAEFGTECYSLNKTVDVSGNCGISDGYTTOCEADNL 540
Qy 540 QCGKLCIKYVKGKFLQIPRATIIYANISGHLCIAVEFASDHADQKWKIDGTSCGSNKV 599
Db 541 QCGKLCIKYVKGKFLQIPRATIIYANISGHLCIAVEFASDHADQKWKIDGTSCGSNKV 600
Qy 600 CRNQRVSSSYLVGVDCTDKNDRGVGNKKGCHCSASYLPDQCSVSDMLWPGSGISDGN 659
Db 601 CKNRQVSSSYLVGVDCTDKNDRGVGNKKGCHCSASYLPDQCSVSDMLWPGSGISDGN 660
Qy 660 PFPVAPARLPERVNIYHVKPMRWPFLLFIPFIIFCVLIAIMVKVNFQKRWKTED 719
Db 661 PFLVAVPARLPERHNMENYHVKPMRWPFLLFIPFIIFCVLIAIMVKVNFQKRWKTED 720
Qy 720 YSSDEQPESESEPKG 734
Db 721 YSSDEQPESESEPKG 735
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RESULT 3

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Q6P2G0 ID Q6P2G0 PRELIMINARY; PRT; 579 AA.
AC Q6P2G0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ADAM2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Cunatrine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064547; AAH64547.1; -
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
SQ SEQUENCE 579 AA; 64795 MW; 1F7AF0CDA2A064F9 CRC64;

Query Match 76.9%; Score 3065.5; DB 2; Length 579;
Best Local Similarity 78.5%; Pred. No. 3.1e-200;
Matches 577; Conservative 0; Mismatches 1; Indels 157; Gaps 3;
Qy 1 MW-VLFLSLGLGLRMDNSFSLPQVITVPEKIRSIIEKIEGIESQASYKIVIEGKPYTVNL 59
Db 1 MWRVFLSLGLGLRMDNSFSLPQVITVPEKIRSIIEKIEGIESQASYKIVIEGKPYTVNL 60
Qy 60 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHVQYIEGYPKSVVMVSTCTGLRGVLQF 119
Db 61 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHVQYIEGYPKSVVMVSTCTGLRGVLQF 120
Qy 120 ENVSYGIEPLESSVGFPEHVIYQVKKADVSLYNEKDIESRDLSEKLSQAEPOODFAKYI 179
Db 121 ENVSYGIEPLESSVGFPEHVIYQVKKADVSLYNEKDIESRDLSEKLSQAEPOODFAKYI 171
Qy 180 EMHVIVEKQLYNNHMGSDTTTVAQVFLIGLITNAIFVSNITILSLSELEWIDENKIATT 239
Db 172 ----- 171
Qy 240 GEANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYGATFOGKMCNDANYAGGVLLHPR 299
Db 172 -----HPR 174
Qy 300 TISLESIAVILAOQLLSLMSGITYDDINKCQCSGAVCIIMNPEAIFHSGVKIFSNCSFEDFA 359
Db 175 TISLESIAVILAOQLLSLMSGITYDDINKCQCSGAVCIIMNPEAIFHSGVKIFSNCSFEDFA 234
Qy 360 HFISKQSKQCLHNPRLDPPFKQAVCGNKLAGEECDCGTEQDCALIGETCCDIATCR 419
Db 235 HFISKQSKQCLHNPRLDPPFKQAVCGNKLAGEECDCGTEQDCALIGETCCDIATCR 294
Qy 420 FKAGSNCAEGPCCNCLFMSKERMCRPSFECDLPYCNCGSSASCENHYVQTGHPCGLN 479
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Db 295 FASGNCAGGCCNCLPMSKRCRPSFECDDLPYCNCGSSASCENHYVQTGHPCCGLN 354
Qy 480 QWICIDGCMGDKQCTDTDFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNL 539
Db 355 QWICIDGCMGDKQCTDTDFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEAD-- 412
Qy 540 QCGKLIKCYVGFLLQIPRATIIYANISGHLCTAVEFASDHADSKQKWKIDGTS CGSNKV 599
Db 413 -----GHLCTAVEFASDHADSKQKWKIDGTS CGSNKV 444
Qy 600 CRNORCVSSSYLGYDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLMPGGSIDSGN 659
Db 445 CRNORCVSSSYLGYDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLMPGGSIDSGN 504
Qy 660 FPPVAIPARLPERRYENIYHSPKMRPFFLFPFFIIFCVLIAMVKVNFQRKKWRTED 719
Db 505 FPPVAIPARLPERRYENIYHSPKMRPFFLFPFFIIFCVLIAMVKVNFQRKKWRTED 564
Qy 720 YSSDEQPESESEPKG 734
Db 565 YSSDEQPESESEPKG 579

RESULT 4
ID AAH64547 PRELIMINARY; PRT; 579 AA.
AC AAH64547;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE ADAM2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Strausberg R.;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064547; AAH64547.1; -
SQ SEQUENCE 579 AA; 64795 MW; 187AF0CDA2A064F9 CRC64;

Query Match 76.9%; Score 3065.5; DB 2; Length 579;
Best Local Similarity 78.5%; Pred. No. 3.1e-200;
Matches 577; Conservative 0; Mismatches 1; Indels 157; Gaps 3;

Qy 1 MW-VLFLSLGLGGLRMDNSFSLPVQITVPEKIRSIIEKIESQASYKIVIEGKPYTNL 59

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Db 1 MWRVLFLLSLGLGGLRMDNSFSLPVQITVPEKIRSIIEKIESQASYKIVIEGKPYTNL 60
Qy 60 MQKNFLPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF 119
Db 61 MQKNFLPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQF 120
Qy 120 ENVSYGIEPLESSVGFHFHYVQVKKADVSLVNEKDIESRDLSEFKUQABPQODFAKYI 179
Db 121 ENVSYGIEPLESSVGFHFHYVQVKKADVSLVNEKDIESRDLSEFKUQABPQODFAKYI 171
Qy 180 EMHVIVEKQLYNHMGSDTTVVAQKVFQILGLTNAIFVSPNITITLSSLELWIDENKATTT 239
Db 172 -----
Qy 240 GEANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVVGATFQGMCDANDYAGGVWLHPR 299
Db 172 -----HPR 174
Qy 300 TISLESIAVILAQLLSMGITVDDINKCOCGAVCINMPEATHFSGVKIFSNCSFEDFA 359
Db 175 TISLESIAVILAQLLSMGITVDDINKCOCGAVCINMPEATHFSGVKIFSNCSFEDFA 234
Qy 360 HFTSKQKSOCLHNQPRLDPPFKQAVCNKAKLEAGEECDCGTEQDCALIGETCCDIATCR 419
Db 235 HFTSKQKSOCLHNQPRLDPPFKQAVCNKAKLEAGEECDCGTEQDCALIGETCCDIATCR 294
Qy 420 FKAGSNCAEGPCCENCLFMSKRCRPSFECDDLPEYCNCGSSASCENHYVQTGHPCCGLN 479
Db 295 FKAGSNCAEGPCCENCLFMSKRCRPSFECDDLPEYCNCGSSASCENHYVQTGHPCCGLN 354
Qy 480 QWICIDGCMGDKQCTDTDFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNL 539
Db 355 QWICIDGCMGDKQCTDTDFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEAD-- 412
Qy 540 QCGKLIKCYVGFLLQIPRATIIYANISGHLCTAVEFASDHADSKQKWKIDGTS CGSNKV 599
Db 413 -----GHLCTAVEFASDHADSKQKWKIDGTS CGSNKV 444
Qy 600 CRNORCVSSSYLGYDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLMPGGSIDSGN 659
Db 445 CRNORCVSSSYLGYDCTTDCNDRGVNCKKHCHCSASYLPPDCSVOSDLMPGGSIDSGN 504
Qy 660 FPPVAIPARLPERRYENIYHSPKMRPFFLFPFFIIFCVLIAMVKVNFQRKKWRTED 719
Db 505 FPPVAIPARLPERRYENIYHSPKMRPFFLFPFFIIFCVLIAMVKVNFQRKKWRTED 564
Qy 720 YSSDEQPESESEPKG 734
Db 565 YSSDEQPESESEPKG 579

RESULT 5
Q866A8
ID Q866A8 PRELIMINARY; PRT; 735 AA.
AC Q866A8;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fertilin beta.
GN Name=FTNB;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22872989; PubMed=14510675;
RA Day A.E., Quilter C.R., Sargent C.A., Mileham A.J.;
RT "Chromosomal mapping, sequence and transcription analysis of the
RT porcine fertilin beta gene (ADAM2).";
RL Anim. Genet. 34:375-378 (2003).

```

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[2]
SEQUENCE FROM: N.A.
RP TISSUE-Testis;
RA Day A.; (2004), Department of Applied Sciences, Anglia Polytechnic
RL University, Cambridge, United Kingdom.
DR EMBL; AJ309003; CAC84225.2; -.
DR HSP; P18619; 1FVL.
DR MEROPS; M12.950; -.
DR GO; GO:004322; F:metalloendopeptidase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR00742; EGF 2.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR008994; Nucleic_acid OB.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep.M12B_propep; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS0215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS0214; DISINTEGRIN_2; 1.
DR PROSITE; PS0026; EGF_3; 1.
SQ SEQUENCE 735 AA; 81804 MW; 16F5554690A8F4AE CRC64;

Query Match 70.8%; Score 2820; DB 2; Length 735;
Best Local Similarity 68.6%; Pred. No. 2.1e-183;
Matches 502; Conservative 96; Mismatches 132; Indels 2; Gaps 2;

QY 3 VLFLLSGLGLRMDNFDSPVQITVPEKRSIIKEGIESQASKIVIEGKPYTNLMQK 62
DB 4 LFLFLIGLGLQADSSERLRVQITVPEKIRISSEGVESHVSNIIIEGKTYTNLVQK 63

QY 63 NLPNFRVSYSGTGMKPDQFQNFCHQVIEGPKSVVMVSTCTGLRGLQFENV 122
DB 64 SFLPHNFRVYNGTNGMKPLEQFQNFCHQVIEGPKSVVMVSTCTGLRGLQFENV 123

QY 123 SYGIEPLESSVGFHVIYQVKKADVSLYNEKDIESRDLSEFKLSAEPPQDFAKYTEH 182
DB 124 SYGIEPLESSVGFHVIYQVKKADVSLYNEKDIESRDLSEFKLSAEPPQDFAKYTEH 183

QY 183 VIVEKQLYNHMGSDTTVAQVQFQIGLTNAIFVSFNITILSLLELWIDENKIATTGEA 242
DB 184 IVEKQLYNHMGSDTTVAQVQFQIGLTNAIFVSFNITILSLLELWIDENKIATTGEA 243

QY 243 NELLHFLRWKTSVLVLRPHDVAFLVYREKSNVVGATFQGMCDANYAGGVVLPHTIS 302
DB 244 NELLHFLRWKTSVLVLRPHDVAFLVYREKSNVVGATFQGMCDANYAGGVVLPHTIS 303

QY 303 LESLAVILAQLLSLGMITTDINKKCCSGAVCTMNPFAHFSQVVKI FSNCSFEDEAFHI 362
DB 304 LESLAVILAQLLSLGMITTDINKKCCSGAVCTMNPFAHFSQVVKI FSNCSFEDEAFHI 363

QY 363 SKQSQCILHNPRLDPFFKQAVCGNAKLEAGEBCDCGTEQDICALIGTCDDIATCFKA 422
DB 364 AKSQCILHNPRLDPFFKQAVCGNAKLEAGEBCDCGTEQDICALIGTCDDIATCFKA 422

QY 423 GSNCAEGPCCNCLFMSEKRCRSPFECDLPEYCNKSSASCPENHYVQTHCPGLNQWI 482
DB 423 GSNCAEGPCCNCLFMSEKRCRSPFECDLPEYCNKSSASCPENHYVQTHCPGLNQWI 482

QY 483 CIDGVCMSGDKQCTDTTFCGEVGFSPSECYSHLNSKTDVSGNCGTSDSGYTCCEADNLQCG 542
DB 483 CIDGVCMSGDKQCTDTTFCGEVGFSPSECYSHLNSKTDVSGNCGTSDSGYTCCEADNLQCG 542

543 KLICKYVGKFLQIPRATIIYANISHLCLIAVEFASDHADSQKQWIKDGTSCSNKVCVN 602
DB 543 KLICKYVGKFLQIPRATIIYANISHLCLIAVEFASDHADSQKQWIKDGTSCSNKVCVN 602

603 QRCVSSSYLYGCTTDCNDRGVCNKKKCHCSASYLPDPCSVQSDLPWCGSDSGNFPP 662
DB 603 KRCIDSSYLYNDCTAEKCHNQGVCNKKRCHCKPTLPPNCEVSVSWPVGSDSGNFPP 662

663 VAIP-ARLPERRYENIYHSPKMRWPFPIFPPIFFICVLIAIMVKVNFORKKWRTEYDYS 721
DB 663 AADPLFGVPRDRIYENIYHSPKMRWPFPIFPPIFFICVLIAIMVKVNFORKKWRTEYDYS 722

722 SDEQSESESEPK 733
DB 723 SDEQSESESETK 734

RESULT 6
AD02_BOVIN STANDARD; PRT; 745 AA.
ID AD02_BOVIN STANDARD; PRT; 745 AA.
AC 077780;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUN-2004 (Rel. 44, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloprotease domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
GN Name=ADAM2; Synonyms=FTNB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=97304362; PubMed=9160725;
RA Waters S.I., White J.M.;
RT "Biochemical and molecular characterization of bovine fertilin alpha
RT and beta (ADAM 1 and ADAM 2): a candidate sperm-egg binding/fusion
RT complex.";
RL Biol. Reprod. 56:1245-1254(1997).
CC -!- FUNCTION: Sperm surface membrane protein that may be involved in
CC sperm-egg plasma membrane adhesion and fusion during
CC fertilization. Could have a direct role in sperm-zona binding or
CC migration of sperm from the uterus into the oviduct. Interactions
CC with egg membrane could be mediated via binding between its
CC disintegrin-like domain to one or more integrins receptors on the
CC egg. This is a non catalytic metalloprotease-like protein (By
CC similarity).
CC -!- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -!- DOMAIN: A tripeptide motif (TDE) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding (By similarity).
CC -!- PTM: The signal and the metalloprotease domain are cleaved during
CC the epididymal maturation of the spermatozoa (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC
CC EMBL; AF086808; AAC62753.1; -.
CC HSP; P18619; 1FVL.
CC MEROPS; M12.950; -.
CC InterPro; IPR006586; ADAM_cysteine.

```

DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR008994; Nucleic acid OB.
 DR InterPro; IPR001590; Peptidase M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00215; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS00214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 16 Potential.
 FT PROPEP 17 174 By similarity.
 FT CHAIN 175 745 ADAM 2.
 FT DOMAIN 17 696 Extracellular (Potential).
 FT TRANSMEM 697 717 Potential.
 FT DOMAIN 718 745 Cytoplasmic (Potential).
 FT DOMAIN 175 382 Metalloprotease-like.
 FT DOMAIN 383 474 Disintegrin-like.
 FT DOMAIN 475 605 Cys-rich.
 FT DOMAIN 611 644 EGF-like.
 FT DOMAIN 148 151 Poly-Ser.
 FT DISULFID 287 370 By similarity.
 FT DISULFID 329 354 By similarity.
 FT DISULFID 444 457 Potential.
 FT DISULFID 615 626 By similarity.
 FT DISULFID 620 632 By similarity.
 FT DISULFID 634 643 By similarity.
 FT CARBOHYD 122 122 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 220 220 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 353 353 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 458 458 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 558 558 N-linked (GLCNAC. .) (Potential).
 SQ SEQUENCE 745 AA; 83150 MW; B5D8DC0168999800 CRC64;
 Query Match 68.3%; Score 2723; DB 1; Length 745;
 Best Local Similarity 64.8%; Pred.No. 8.4e-177;
 Matches 481; Conservative 103; Mismatches 146; Indels 12; Gaps 2;
 QY 3 VLFLLSGLGLRMSDFSLVQITVPEKIRSIKEGIESQASYKIVIEGKPYTVNLMQK 62
 DB 4 LFLLLGLTGLQTDNLSERLRVQTVPEKIRSTSSGGVETHSVIILIEGKTYTVNLMQK 63
 QY 63 NFLPHFRVSYSGTGIMKPLDQDFQNFCHYQYIEGPKSVVMVSTCTGLRGVLPENY 122
 DB 64 AFLPHFRVSYSGTGSMKPLEHEFQNFYQYQYIEGPKSVMAIISTCTGLRGVLPENY 123
 QY 123 SYGIEPLESSVGPEHVIYQVKKKADVSLNEXDKIESRDLSPKLSQAEPOODFAKVIEMH 182
 DB 124 SYGIEPLESGIEGHEVMYQIKPDSSSSVTEREIEURKPKYQNVPELPDPSQVIEHM 183
 QY 183 VIVEKOLYNHMGSDTTVAQVFLQIGLTNAIVFSFNITILSLSLWIDENKIATGGA 242
 DB 184 IVEKOLYNHMGADTTVVIQIKIQLTGLTNAITSLNITVLSLWIDENKIPTGDA 243
 QY 243 NELLHTFLRWKTSYVLRLPHDVAFLVLYREKSNVYGATFGKWCNDANYAGVVLHPTIS 302
 DB 244 NELLHFRVKKRSYVLRLPHDMAFLVLYREKSNYIGATFGQRCMDKHGGVGLHSSIS 303
 QY 303 LESLAVILAQLLSLWIGTIVDDINKKCCSACVIMNPEATHFSGVKIFSNCSFEDFAHI 362
 DB 304 LESLAVIIAQLLSLWIGIPYDDINKKCHCPGDVIMNPAAVHSSGVKLFNSCVDDELRFI 363

QY 363 SKOKSOCLHNQPRLDFFFKQOAVCGNAKLEAGBECDCGTQDCCALIGETCCDIATCRFKA 422
 DB 364 SKPKSOCLNQPRLDPTYK-SAVCGNGKVEBQCCGCKKACDALPDTCCVADTCRPOP 422
 QY 423 GSNCAESGPCCECLFWSKERMCPSPEECDLPYCNCGSSASCENHYVOTGHPGCLNQWI 482
 DB 423 GSACDTGLCCESCAFIPKGHICRGSTDECDLHYICNGSSAACQEDVYVQDHPGCGNQWL 482
 QY 483 CIDGVCMGSKQCTDTFGKEVEFGPECYSHLNSKTVDVSGNCGISDSGYTQCEADNLQCG 542
 DB 483 CIGSICVDGIGKQCFDIFGEGTSYAPAECFORLNSMNDLSCNGCVTPGTPTCTSENVRG 542
 QY 543 KLICKYVKGELLQIPRATIIYANISGHLCTIAVFASDHADSQKWIKDGTSKCSNKKVCRN 602
 DB 543 KLLCTYDKREVISVENASVMYSNKGKICIGLHYEGNEDEGMMVWKDGTVCGESKICQN 602
 QY 603 QRCVSSSYLGVDCTTDKCDNRGVCKNKKCHCSASYLPDSCSVQSDLWPGSSIDSGNFP 662
 DB 603 QKCVSSFLNYDCNPKCNQGVCKNKKCHCPSYLPFNCEHSAPGWEKIDSGNFP 662
 QY 663 VAIP-----ARLPERRYENIYHSKPMRWPFFLPIFFIIFCVLIAIMVKVNFQ 711
 DB 663 SEPTGPAFTDVGTTPLAESRYIENVRSKPTRWPFPIFFIIFCVLIAIATLVKYVQ 722
 QY 712 RKXWRTEDYSSDQPSSESEPK 733
 DB 723 RKXWRTEDYSSDQPSSESEPK 744
 RESULT 7
 AD02_RABIT STANDARD; PRT; 751 AA.
 AC Q28660;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 03-JUN-2004 (Rel. 44, Last annotation update)
 DE ADAM 2 precursor (A disintegrin and metalloprotease domain 2)
 DE (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
 GN Name=ADAM2; Synonyms=FTNB;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97071141; PubMed=8914066;
 RA Hardy C.M., Holland M.K.;
 RT "Cloning and expression of recombinant rabbit fertilin.";
 RL Mol. Reprod. Dev. 45:107-116(1996).
 CC -!- FUNCTION: Sperm surface membrane protein that may be involved in
 CC sperm-egg plasma membrane adhesion and fusion during
 CC fertilization. Could have a direct role in sperm-zona binding or
 CC migration of sperm from the uterus into the oviduct. Interactions
 CC with egg membrane could be mediated via binding between its
 CC disintegrin-like domain to one or more integrins receptors on the
 CC egg. This is a non catalytic metalloprotease-like protein (By
 CC similarity).
 CC -!- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed specifically in testis.
 CC -!- DOMAIN: A tripeptide motif (VGE) within disintegrin-like domain
 CC could be involved in the binding to egg integrin receptor and thus
 CC could mediate sperm/egg binding (By similarity).
 CC -!- PTM: The signal and the metalloprotease domain are cleaved during
 CC the epididymal maturation of the spermatozoa (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M12B.
 CC -!- SIMILARITY: Contains 1 disintegrin domain.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -----
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CC EMBL; U46070; AAA93321.1; -;
 CC HSSP; P30403; INAY.
 DR MEROPS; M12.950; -;
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR008994; Nucleic acid OB.
 DR InterPro; IPR001590; Peptidase M12B.
 DR InterPro; IPR002870; Peptidase M12B_N.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR PRODOM; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE NEG.
 DR PROSITE; PS01186; EGF_2; FALSE NEG.
 DR PROSITE; PS50026; EGF_3; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 16 Potential.
 FT PROPEP 17 173 By similarity.
 FT CHAIN 17 751 ADAM 2.
 FT DOMAIN 17 702 Extracellular (Potential).
 FT TRANSMEM 703 723 Potential.
 FT DOMAIN 724 751 Cytoplasmic (Potential).
 FT DOMAIN 174 381 Disintegrin-like.
 FT DOMAIN 382 474 Cys-rich.
 FT DOMAIN 475 606 EGF-like.
 FT DOMAIN 612 645 By similarity.
 FT DISULFID 286 369 By similarity.
 FT DISULFID 328 353 Potential.
 FT DISULFID 444 457 Potential.
 FT DISULFID 616 627 By similarity.
 FT DISULFID 621 633 By similarity.
 FT DISULFID 635 644 By similarity.
 FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 219 219 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 352 352 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 559 559 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 566 566 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 643 643 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 751 AA; 83616 MW; 824C6FBFC4A9FCE1 CRC64;
 Query Match 67.4%; Score 2685; DB 1; Length 751;
 Best Local Similarity 64.4%; Pred. No. 3.3e-174;
 Matches 482; Conservative 106; Mismatches 142; Indels 18; Gaps 4;
 QY 3 VLFLSLGLGLRMDNFDLSLQVITPEKRSIIKEGIESQASQKIVIEGKPYTVNLQMQK 62
 DB 4 VLFLSLGLSLGRKENSERLHVQVTPVKMRSVTSEGFTEVNVNIVIEGKTYTLNLQMQK 63
 QY 63 NPLPHRNVYSYSGTGMKPLDQDFQNFCHQYHIEGYPKSVVMVSTCTGLRGLQFENV 122
 DB 64 LFLPDRFRVGYDSTGMKLEQDFQNFCHQYHIEGYPKSVVMVSTCTGLRGLQFENV 123
 QY 123 SYGIEPLESSVGFPHVYQVKKADVSLYNEKDIESRDLSPKLSQAEPOQDFAKYIEMH 182
 DB 124 TYGIEPLESSIGFPHVYQVKKADVSLYNEKDIESRDLSPKLSQAEPOQDFAKYIEMH 182

QY 183 VIVEKOLYNHMGSDTTVAQKVFQQLIGLTNAIFVSNFTIILSSLELWIDENKIATCEA 242
 DB 183 VVVEKNLYKMGSDTAVVSKIFQQLIGLTNAVFTSNFTIILSSLELWIDENKISTTGA 242
 QY 243 NELLHTPLRWKTSYLVLRPHDVAFLVYREKSNVVGATFQGMCDKMDANYAGVVLHPKTI 302
 DB 243 NELLYRFLRWKTSYLVLRPHDVAFLVYREKSNVVGATFQGMCDKMDANYAGVVLHPKTI 302
 QY 303 LESLAVILAOLLSISMGITVDDINKKOCSCGAVCIMNPEATHFSQVKIFSNCSPEDEFAHFI 362
 DB 303 LESLAVILAOLLSISMGITVDDINKKOCSCGAVCIMNPEATHFSQVKIFSNCSPEDEFAHFI 362
 QY 363 SKOKSQCQLHNPRLDPPFFKQQAACVGNKLEAGBECDCGTEDQDCALIGETCCDIATCRFKA 422
 DB 363 SKOKSQCQLHNPRLDPPFFKQQAACVGNKLEAGBECDCGTEDQDCALIGETCCDIATCRFKA 422
 QY 423 GSNCAEGPCCECNCLFMSKERMCRPSFEEDLPYCNCGSSASCENHYVQTHGPCGLNQWI 482
 DB 423 GSNCAEGPCCECNCLFMSKERMCRPSFEEDLPYCNCGSSASCENHYVQTHGPCGLNQWI 482
 QY 483 CIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTD-VSGNGCISDSGYTQCEADNLQC 541
 DB 483 CIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTD-VSGNGCISDSGYTQCEADNLQC 541
 QY 542 GKLICKYVGVKFLQIPRATIIYANISGHLCIAVEFASDHADSKQMWIKDGTSCGSKNVCR 601
 DB 542 GKLICKYVGVKFLQIPRATIIYANISGHLCIAVEFASDHADSKQMWIKDGTSCGSKNVCR 601
 QY 602 NQRCVSSSYGYDCTTDKCNDRGVNKKKHCHCSASYLPDPCVSQSDLPWGGSIDGNF- 660
 DB 602 NQRCVSSSYGYDCTTDKCNDRGVNKKKHCHCSASYLPDPCVSQSDLPWGGSIDGNF- 660
 QY 661 -----PPVAIPARLPERRYENIYH-SKPMWPPFLRTPPFIIFCVLIAM 705
 DB 661 -----PPVAIPARLPERRYENIYH-SKPMWPPFLRTPPFIIFCVLIAM 705
 QY 706 KYNVORKKWRTEYSSDEQSESESEBP 733
 DB 706 KYNVORKKWRTEYSSDEQSESESEBP 733
 QY 723 VKVQFQKWKTEYSSDEQSESESEBP 750
 DB 723 VKVQFQKWKTEYSSDEQSESESEBP 750
 RESULT 8
 ID AD02 RAT STANDARD; PRT; 737 AA.
 AC Q63202;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
 GN (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=98019039; PubMed=9358007;
 RA McLaughlin E.A., Frayne J., Barker H.L., Jury J.A., Jones R.,
 RA Ford W.C.L., Hall L.;
 RT "Cloning and sequence analysis of rat fertilin alpha and beta -
 RL Mol. Hum. Reprod. 3:801-809(1997).
 CC -!- FUNCTION: Sperm surface membrane protein that may be involved in
 CC sperm-egg plasma membrane adhesion and fusion during
 CC fertilization. Could have a direct role in sperm-zona binding or
 CC migration of sperm from the uterus into the oviduct. Interactions
 CC with egg membrane could be mediated via binding between its
 CC disintegrin-like domain to one or more integrins receptors on the
 CC egg. This is a non catalytic metalloprotease-like protein (By
 CC similarity).
 CC -!- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.

Matches	442;	Conservative	119;	Mismatches	166;	Indels	13;	Gaps	8
Qy	1	MW-VLFLLSG---	LGGL---	RMDSNFDSP	LVQITVPEKIRSIIRKEGIESQAS	YIVIEGK	53		
Db	1	MWILLLLSGLSELGGL	SQSQTG	REKRLHVQTVPEKIRSVTSNG	YETQVTYNLKIEGK	60			
Qy	54	PYTVNLQKQFLPNFRVYS	SGTGMKPLDQDFQNFCHYQGYEGY	PGPKSVVMKSTCTGL	113				
Db	61	TYTLDLQKQFLPNFRVYS	YDNAGIMRSLBQFNICYFOGYEGY	PNSMVIYSTCTGL	120				
Qy	114	RGVLQFENVSGIPELSS	VGFEHVIYQVHKHKADVSLYNEKDI	ESRDLSPKLSAEPQQ	173				
Db	121	RGFLQFGNVSGIPELSS	VGFEHVIYQVEPEKGALLYAEKIDLRDSQ	TKIRSIKRP	180				
Qy	174	DFAKYIEMHVIIVERQ	LNYHMGSDTTVVAQKVQLIGLTNAIFV	SFNITIIILSSLELWIDE	233				
Db	181	IVSHYLEIHIIVEXQ	MEHIGADTAIVTKIFQLIGLANAIFAPNL	TVILSSLEFWMDE	240				
Qy	234	NKIATTGEANELLTF	RLWTKTSYLVRPHDVAFLLVTRKSNY	VGATFGQKMDANVAGG	293				
Db	241	NKILTTGDANKLLY	RLFKNWQSYLVLRPHDMAFLLVYRNT	TDYVGATYQGWCDKNVAGG	300				
Qy	294	VVLHPRTISLES	LAQILLSLSMGITYDDINKCOCSGAVCI	MNPEAIHESGVKISNC	353				
Db	301	VALHPKAVTLE	SLAIIIVQLLSLMSGLAYDNNKCCQGP	VCVMNPEAPHS	SGVRAFNSC	360			
Qy	354	SFEDFAHFISKQ	SQCLHNQRLDPFFKQQAQVCGNAKLE	AGEEDCCGTEQD	CALIGETCC	413			
Db	361	SMEDFSKFI	TSOSSHCLQNQLPSYK-MAVCG	NGEVEDEICDG-KKCAEM	PPPC	418			
Qy	414	DIATCRFKAGS	NCABGCCENCLFMSKERMCRPSF	EBCDLPEYCN	SGSASCENHYVOTG	473			
Db	419	NPDTCKLS	SDGSECSGGICCNCKLRKGEVCRLAQ	DECDVTEYCNGTSEVC-EDFFV	QNG	477			
Qy	474	HPCLGNQWICIDG	VCMSDKQCTTFTEGKEVFEFGSECV	SHLSKTDYSGNGCIS	DSGYQ	533			
Db	478	HPCDNRRKVIC	NGTCQSGEQOQDLFGIDAGFGS	SECFWELNSKDISG	SGCISAGGYKE	537			
Qy	534	CEADNLQCGK	LICKYVGKFLIQIPRATIIYANIS	GHLCIAVEFASDIAD	SOKMKIDGTS	593			
Db	538	CPPNDRMCGK	LICKYQSENILKURSATVIYANIS	GHVCSVLEYEQGHNESQ	GMVRDGTV	597			
Qy	594	CGSNKVCNRQ	RCVSSYGLYDCTTDKCDNRGVCNNK	KKCHCSASYLPPDCSV	QSDLMPGG	653			
Db	598	CGSNKVCNQK	CVADTFELGYDCNLEKCNHGV	CNNKKNCHDPTLPPDCK	RMKDSYFGG	657			
Qy	654	SIDSGNPPV	PAIPARLPERRIENIYHSKPMRW	PFPIFPIFCVLIAIMVKV	QNRK	713			
Db	658	SIDSGN-KERAEP-	-IPVRPYIASAYRSKSPRWPF	FLIIPYVILVILGLMLV	KVYSQRM	714			
Qy	714	KWRTEYSS	DEQPESESEPK	733					
Db	715	KWRMDFS	SESESESESK	734					
RESULT 10									
AD02_CAVPO									
ID	AD02	CAVPO	STANDARD;	PRT;	735	AA.			
AC	Q60411;								
DT	28-FEB-2003	(Rel. 41, Created)							
DT	28-FEB-2003	(Rel. 41, Last sequence update)							
DT	05-JUL-2004	(Rel. 44, Last annotation update)							
DE	ADAM 2 precursor	A disintegrin and metalloproteinase domain 2							
DE	(Fertilin beta subunit)	(PH-30) (PH30).							
GN	Name=ADAM2;	Synonyms=FTNB;							
OS	Cavia porcellus	(Guinea pig).							
OC	Eukaryota;	Metazoa;	Chordata;						
OC	Mammalia;	Eutheria;	Rodentia;						
OX	NCBI_TaxID=10141;								
RP	[1]								
RN	SEQUENCE FROM N.A.								
RC	TISSUE=Testis;								
RX	MEDLINE=94069486;	PubMed=9248170;							

FT DOMAIN 184 389 Metalloprotease-like.
FT DOMAIN 390 479 Disintegrin-like.
FT DOMAIN 480 619 Cys-rich.
FT DOMAIN 620 654 EGF-like.
FT DISULFID 293 376 By similarity.
FT DISULFID 335 360 By similarity.
FT DISULFID 458 483 Potential.
FT DISULFID 624 636 By similarity.
FT DISULFID 630 642 By similarity.
FT DISULFID 644 653 By similarity.
FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 149 149 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 156 156 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 294 294 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 359 359 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 465 465 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 611 611 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 625 625 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 746 AA; 84448 MW; 1D8C7E9071502E30 CRC64;
Query Match 39.8%; Score 1586.5; DB 1; Length 746;
Best Local Similarity 42.4%; Pred.No.1:9e-99;
Matches 310; Conservative 125; Mismatches 261; Indels 35; Gaps 12;
Qy 2 WVLFLSLGLRMDNSFSLPQVITPEKIRSIIEKIEGIESOASYKIVIEGKPYTNLMQ 61
Db 3 FLALLTELRLQAHVSGSEGLFHVTVPRKLSNDSSEVSRKMIYITIDGQPYTLHLK 62
Qy 62 KNFLPHNFRVSYSGTGMKPLDQDFQNFHYGYIEGYPKSVVWVSTCTGLRGVLFQFN 121
Db 63 QSELPQNFVLYTNEAGLSHSESPFYMHHCHYGAYAAFPNSFVTLSCSLRGLFQFN 122
Qy 122 VSGIEPLESSVGEHVHYGVKKKADVSLY--NEKDIESRDLSPKLOSAEPQDPFAK-- 177
Db 123 VSGIEPLESSARPEHIYQMKNDPNVSIENYSHIWQDOSYKVPILNSQKXNLSKLL 182
Qy 178 --YIEMHIVKQLYNHMGSDTTVAQVFLQGLTNAIFVFNITILSLSLWIDENK 235
Db 183 PQYLEIIVIEKALDYMGSEMAVTKIVQVIGLVNTMTQFLTLVLSLSLWSNENQ 242
Qy 236 IATGEANELLHLFLRWKTSYLVLRPHDAFLVLYREKSNVYGATPGKMKCDANYAGVV 295
Db 243 ISTSGDADDLQRLAWKRDYLLRPHDIAYLLVYRKHYPYVGATPGTTCNESYDAGIA 302
Qy 296 LHPTISLESIAVLAQLLSLWGITYDDINKOCGCAVCMMPKPAETHFSGVIFPNCSP 355
Db 303 MYDAIDLEGFSVILIAQLLGLNVGLTYDDITQCFLRATCMNHENASARGIKFNSCM 362
Qy 356 EDFAHFIKSKOCLHNQPRLDPPFKQAVCGNAKLEAGBECDCGTQDCALIGETCCDI 415
Db 363 HDYRYFVSKFEAKCLQKLSNLQPLHONQVCGNIGLESNEECDCGNKKECF--KKCCDY 420
Qy 416 ATCRFKAGSNAEGPCC--ENCLFMKSKRMCRPSE--ECDLPYVCGSSASCENHYVQTG 473
Db 421 NTCKLKGSVKCGSPCCSTSKELSVGTPCRKSVDPCECTEYCNGTSGSDCPVPTALNG 480
Qy 474 HPCLNLQMI CIDGVCMSGDQCTDTFGKEVEFGPSECYSHLNSKTYDSNGCGISDSGYTQ 533
Db 481 HLCKLGTAYCYNGOCQDTNQCAKIFGKGAQGFACFCFKVNSLHETSENGCFKNSQPLP 540
Qy 534 CEADNLQCKGLIKYVKGKFLQIPRATIIIVANTSGHLICIAV---EPASDHADSOQKWK 589
Db 541 CERKDVLCGLKACVQPHNAYKSDIQYTVSYIQDVCHVCIATGSSNRSGTDN--AYVA 598
Qy 590 DGTSCGNKVCNRCORCVSSSYLGYDC--TTDKCNDRGVCKNKKCHCASYLPPDCSVQSD 648
Db 599 DGTWCGPEYCVNKTCKRVHLTGNCNTTKCKGKGCNNFGNQCQPPGKHPDCKPQFG 658
Qy 649 LWPFGSIDSGNFPFVATPARLPERYIENYHSPKRW---PPFLFTPFPIIFCVLIAM 705
Db 659 S-PGGSIDGDNF-----QKSDEFYTEKGYNAHNNWNFTLSFVILVFPFIITFIVI--- 707

Qy 706 VKVNFQKKWR 716
Db 708 ----FKRNEIR 714
RESULT 12
AD18 HUMAN
ID AD18_HUMAN STANDARD; PRT; 739 AA.
AC Q9Y307;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE ADAM 18 precursor (A disintegrin and metalloproteinase domain 18)
DE (Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-rich protein III) (tMDC III).
GN Name=ADAM18; Synonyms=TMDC3;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hall L., Frayne J., Dimsey E.A.;
RT "Nucleotide sequence of the human tMDC III sperm surface protein transcript."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sperm surface membrane protein that may be involved in spermatogenesis and fertilization. This is a non catalytic metalloproteinase-like protein (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -!- DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).
CC -!- PTM: The prodomain and the metalloproteinase-like domain are cleaved during the epididymal maturation of the spermatozoa (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.

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CC EMBL; AJ133004; CAB40812.1; --
CC HSP; P83469; IMPZ.
CC MEROPS; M12.957; --
CC Genew; HGNC:196; ADAM18.
CC GO; GO:0005624; C:membrane fraction; TAS.
CC GO; GO:0008237; F:metalloproteinase activity; TAS.
CC GO; GO:0007283; P:permatogenesis; TAS.
CC InterPro; IPR006586; ADAM cysteine.
CC InterPro; IPR001762; Disintegrin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR002870; Peptidase_M12B.
CC InterPro; IPR001590; Peptidase_M12B.
CC Pfam; PF00200; Disintegrin; 1.
CC Pfam; PF01562; Pep_M12B_propep; 1.
CC Pfam; PF01421; Repolysin; 1.
CC ProDom; PD000664; Disintegrin; 1.
CC SMART; SM00608; ACR; 1.
CC SMART; SM00050; DISIN; 1.
CC PROSITE; PS0215; ADAM_MBP; 1.
CC PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
CC PROSITE; PS0214; DISINTEGRIN_2; 1.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR ENBL; BC026169; AAH26169.1; -
DR ENBL; BC028702; AAH28702.1; -
DR ENBL; BC030014; AAH30014.1; -
DR ENBL; BC030698; AAH30698.1; -
DR ENBL; BC034975; AAH34975.1; -
DR ENBL; AV358739; AA089099.1; -
DR HSPP; P30403; IN4Y.
DR MEXOPS; M12.960; -
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR PROSITE; PS0215; ADAM_MEPRO; 1.
DR PROSITE; PS0214; DISINTEGRIN_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00026; EGF_3; 1.
KW Integrin; Metalloprotease; Protease.
SQ SEQUENCE 787 AA; 87933 MW; 3D84CACFECC1A12E CRC64;

Query Match 38.3%; Score 1524.5; DB 2; Length 787;
Best Local Similarity 41.1%; Pred. No. 3.4e-95;
Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18;

QY 1 MWVLLSGLGGLRMD-SNFDSPVQIVTPEKIRSIIEKIEGIE---SQASKYIVIEGKPYT 56
DB 4 LWL--LLAGLCGLLASRPGFQNSLLQIVPEKIQTNTDSSEIEYEQISYIIPIDEKLYT 61

QY 57 VNLMOKNFLPHNFRVSYSGTGIMKPLDQDFONFCHYQVIEGPKSVVWVSTCTGLRGV 116
DB 62 VHLKQRYFLADNFMVLYN-QGSNMTYSSDIQTQCYQGNIEGYPDSMVTLSGSLRGI 120

QY 117 LQFNVSYGIEPLESSVGFHEVIYQVKKADVSLYNEKDIESR---DLGFKLQSAEPQ 173
DB 121 LQFNVSYGIEPLESAVEFQVHLVLYKLNEDNDAIFDRLSKQPMDDNFISEKSEPAV 180

QY 174 D--FQKYMVHVIYVEKOLYNNHMGSDTTVAQKVFQLIQLTNLNAIFVSNITILLSSLELWI 231
DB 181 PDLFPLYLEHIVVDKLYDYGWSDSMIVTNKVIIEVGLANSMTFTQFKVIVLSLELWS 240

QY 232 DENKIATGANELLHTFLRWKTSYLVLRPHDVAFLVIREKSNVYQATGQKMCNDANYA 291
DB 241 DENKISTVGEADELLQKFLWKQSYLRLPHDIAVLLIYMDYPRYLGAFFPGTWCITRYS 300

QY 292 GGVLVHPTTSLSELAVALQLLSLNGITVDDINKCQCGAVCMNPEAHFSGVKIES 351
DB 301 AGVALYPREITLEAFVIVTQMLALSIGIYDDPKKCCSESTCMNPEVQVSGNVTFS 360

QY 352 NCSPEDEFAHTISKQSQCLHNQPLDPFFKQQAQVCGNAKLEAGCECQTEQDCALICET 411
DB 361 SCSLRSQNFVSNVGVKCLQNKPMQOK-KSPKPCVCGNRLGEGNEICDQTEAQCQ--PAS 417

QY 412 CCDIATCRFKAGSNCAEGPCPCENCLFMSKEMRCRP-SFEEDCLPEYCNCGSASCPENHY 470

DB 418 CDFRTRCVLKGAKCYKGLCKDCQILQSGVECRPKAHPCEDIAENCNGSSPECGPDI 477
QY 471 QTGHPCLNMIWICIDGVCMSGDKQCTDTTFOKEVEFGPSECYSHLNSKTYDVGNGCIS-DS 529
DB 478 INGLSCKNNKFCIDGDCDCHLDARCESVFGKSRNAPFACYEETQSOSDRFGNCRDRNN 537
QY 530 GYTQCEADNLQCKLKICKYVGKELLQIPRATIIYANISGHLICIAVEFASDHADSQKWK 589
DB 538 KYVFCGRNRNLCGRVLCVTPYTRKPFHQENGVDVIAFVRDVSVCITVOYKLPRTVPDPLAVK 597
QY 590 DGTSCGNSNKCVRNQRQVSSSYL---GYDCTTDCNDRGVCNNKKGHCSCASLYPPDCSVQ 646
DB 598 NGSCQDGRVNVNRECVESRIIKAHVC-SQSCSGHGVCDNRKCHCSFGYKPPNCOIR 656
QY 647 SLDWPGSI-----DSGNFPFVAIPARLPERRYENIYHSPKMW--PFFLPIFFIIFCV 700
DB 657 S---KGFSIPPEEDMGSI-----MERASGKTENTWLLGLFLIALPILIV--- 696
QY 701 LIAIMVKNFORKWRTEYSSDEQPESESEPKG 734
DB 697 -TTAIVLARKOLKWKFAKE---EEFPSSSEKSEG 726

RESULT 14
AAQ89099 PRELIMINARY; PRT; 787 AA.
AC AAQ89099;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Similar to MDC family.
GN UNQ5982.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR ENBL; AV358739; AA089099.1; -
SQ SEQUENCE 787 AA; 87933 MW; 3D84CACFECC1A12E CRC64;

Query Match 38.3%; Score 1524.5; DB 2; Length 787;
Best Local Similarity 41.1%; Pred. No. 3.4e-95;
Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18;

QY 1 MWVLLSGLGGLRMD-SNFDSPVQIVTPEKIRSIIEKIEGIE---SQASKYIVIEGKPYT 56
DB 4 LWL--LLAGLCGLLASRPGFQNSLLQIVPEKIQTNTDSSEIEYEQISYIIPIDEKLYT 61

QY 57 VNLMOKNFLPHNFRVSYSGTGIMKPLDQDFONFCHYQVIEGPKSVVWVSTCTGLRGV 116
DB 62 VHLKQRYFLADNFMVLYN-QGSNMTYSSDIQTQCYQGNIEGYPDSMVTLSGSLRGI 120

QY 117 LQFNVSYGIEPLESSVGFHEVIYQVKKADVSLYNEKDIESR---DLGFKLQSAEPQ 173
DB 121 LQFNVSYGIEPLESAVEFQVHLVLYKLNEDNDAIFDRLSKQPMDDNFISEKSEPAV 180

QY 174 D--FQKYMVHVIYVEKOLYNNHMGSDTTVAQKVFQLIQLTNLNAIFVSNITILLSSLELWI 231

Db 181 PDLPFLYLEMHVVDKTLTYDYGSDSMIVTNKVIIEVLGANSMTQFKVTIVLSLELWS 240
Qy 232 DENKIATTGEANELHLPRLWKTSLVLRPHDVAFLVYREKSNVVGATFGKWCNDANYA 291
Db 241 DENKISTVGEADELLQKFLWQSLNLRPHDIAVLLIYMDYPRYLGAFFGTWCITRYS 300
Qy 292 GGVLHPRTISLESIAVLAQLLSMIGTYDDINKKQCSGAVCIMMPEAHFSGVKIFS 351
Db 301 AGVALYPKEITLFAFVITQMLALSIGSYDDPKKQCSSESTCIMMPEVQSGVKIFS 360
Qy 352 NCSFEDFAHFTSKQSKQLNQLRDLPPFKQAOVCGNAKLBAEBCDGTQDCCALIGET 411
Db 361 SCSLRSFQNFISVGVKQLQKQPKQK-KSPKPCVCGNGRLEGNEICDGTQEAQCG--PAS 417
Qy 412 CCDIATCRFKAGSNCAEPCENCLFMSKRMCRP-SFEECDLPEYNGSSASCPENHYV 470
Db 418 CCDFRICVLKDGAKYKGLCKCQILQSGVECRPKAHPEDCIAENCGSSPECGPDITL 477
Qy 471 QTGHPCGLNQCWICIDGVCMSGDQCTDTFGKEVFGPSECYSHLNSKTDVSGNCGIS-DS 529
Db 478 INGLSCNNKFCIDYGDCHDLARCESVFGKSRNAPFACVEEIQSQSDRFGNCRDRNN 537
Qy 530 GYTQCEADNLOCGKLIKCYVGFLLQIPRATIIYANISGHICIAVEFASDHADSKMKWIK 589
Db 538 KYVFCGRNLICGLRVCTYPRKPFQENGDIYAFVRDVSVCITVDYKLPRTVPDPLAVK 597
Qy 590 DGTSCGSKVCRNQCYSVSSYL---GYDCTTDKNDRCVGNKCKHCHCSASYLPDQCSVQ 646
Db 598 NGSQCDIGRVCNRECVESRIKASAVC-SQCSGSHGVCDNRNCKHCHCSGPKPKPCOIR 656
Qy 647 SLDLPGGSII----DSGNFPPVPAIPARLPERYIENIYHSPMRV--PFFLIPFPIIFCV 700
Db 657 S---KGFSIPEEDMGSI-----MERASGKTENTWLLGLIALPILIV---696
Qy 701 LIAIMVKNFQKWKRTEDYSSDQPESEBPKG 734
Db 697 -TTAIVLARKQLKWKFAKE---EEFPPSESKSEG 726

RESULT 15
Q8TC42
ID Q8TC42 PRELIMINARY; PRT; 787 AA.
AC Q8TC42;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A disintegrin and metalloprotease domain 32.
GN Name=ADAM32;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McWean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.,
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026085; AAH26085.1; -
DR HSPF; P30403; IN41.
DR MEROPS; M12.960; -
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PSS0215; ADAM_MPRO; 1.
DR PROSITE; PSS0214; DISINTEGRIN 2; 1.
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KW Integrin; Metalloprotease; Protease.
SQ SEQUENCE 787 AA; 87931 MW; CE0F54A50466B336 CRC64;

Query Match 38.1%; Score 1519.5; DB 2; Length 787;
Best Local Similarity 41.0%; Pred. No. 7.5e-95;
Matches 309; Conservative 135; Mismatches 259; Indels 51; Gaps 18;

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Qy 57 VNLQKXNPLPHNFRVSYSGTGIMKPLDQDFQNFCHQYGYIEGPKVVMVSTCTGLRGV 116
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Qy 117 LQFENVSYGIEPLESSVGFPHVYVQVKKKADVSLNEXKDIESR---DLSPKLSQSAEPQ 173
Db 121 LQFENVSYGIEPLESAVEFQHLVLYKLKNEINDIAIFIDRGLKEQPMDDNIFISEKSPAV 180
Qy 174 D--FAKIEHVIKOLYNHMSDITVVAQKVPOLIGLTNAIFVSNITIIISLLEWI 231
Db 181 PDLFPLYLEHVIIVDKTLDYWGSDSMIVTNKVIIEVLGANSMTQFKVTIVLSLELWS 240
Qy 232 DENKIATTGEANELHLPRLWKTSLVLRPHDVAFLVYREKSNVVGATFGKWCNDANYA 291
Db 241 DENKISTVGEADELLQKFLWQSLNLRPHDIAVLLIYMDYPRYLGAFFGTWCITRYS 300
Qy 292 GGVLHPRTISLESIAVLAQLLSMIGTYDDINKKQCSGAVCIMMPEAHFSGVKIFS 351
Db 301 AGVALYPKEITLFAFVITQMLALSIGSYDDPKKQCSSESTCIMMPEVQSGVKIFS 360
Qy 352 NCSFEDFAHFTSKQSKQLNQLRDLPPFKQAOVCGNAKLBAEBCDGTQDCCALIGET 411
Db 361 SCSLRSFQNFISVGVKQLQKQPKQK-KSPKPCVCGNGRLEGNEICDGTQEAQCG--PAS 417
Qy 412 CCDIATCRFKAGSNCAEPCENCLFMSKRMCRP-SFEECDLPEYNGSSASCPENHYV 470
Db 418 CCDFRICVLKDGAKYKGLCKCQILQSGVECRPKAHPEDCIAENCGSSPECGPDITL 477
Qy 471 QTGHPCGLNQCWICIDGVCMSGDQCTDTFGKEVFGPSECYSHLNSKTDVSGNCGIS-DS 529

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Db 478 INGLSCNNKFCYDGDCHDLARCESVFGKGSNAPFACYEETQSQSDRFGNGCRDRNN 537
Qy 530 GYTOCEADNLQCGKLIQKLYGKFLQIPRATIIYANISGHLCTIAVEFASDHADSQKWKIK 589
Db 538 KYVFCGWRNLICGRVCTYPTKPFHQENGDIYAFVRDSCITVDYKLPRTVPDPLAVK 597
Qy 590 DGTSCGSNKYCRNORCVSSYL---GYDCTTDKNDRGVCNNKXKHCHCSASYLPPDCSVQ 646
Db 598 NGSQCDIGRVCVNRCEVSRIIKASAHVC-SQQCSGHGVCDSRNKCHCSPGYKPPNQIR 656
Qy 647 SDLWPGGSI---DSGNFPPVAIPARLPERRYENIYHVKPMRW--PFFLFIPFFIIFCV 700
Db 657 S---KGESIPEEDMGSI-----MERASGKTENTWLLGFLIALPILIV--- 696
Qy 701 LIAMVKVNFQRKQWRTEDYSSDEQPESEPKG 734
Db 697 -TTAIVLARQLKKWFAKE---EEFPSSEKSEG 726
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Job time : 204 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 22:20:47 ; Search time 148 Seconds
(without alignments)
1788.239 Million cell updates/sec

Title: US-10-054-683-19
Perfect score: 3984
Sequence: 1 MWVFLSLGLGRLMDSNFD.....WRTEDYSDEQSESEPKG 734

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues
Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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 - 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
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 - 15: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
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 - 19: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*
 - 20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3984	100.0	734	14	US-10-054-683-19
2	3984	100.0	734	14	US-10-205-823-10
3	3984	100.0	734	17	US-10-473-603-19
4	3969.5	99.6	735	14	US-10-205-823-8
5	3898	97.6	753	14	US-10-205-823-6
6	1524.5	38.3	787	14	US-10-227-884-90
7	1524.5	38.3	787	14	US-10-230-338-90
8	1524.5	38.3	787	14	US-10-218-631-90
9	1524.5	38.3	787	14	US-10-230-414-90
10	1524.5	38.3	787	14	US-10-232-224-90
11	1524.5	38.3	787	14	US-10-216-159A-90
12	1524.5	38.3	787	14	US-10-218-849-90
13	1524.5	38.3	787	14	US-10-218-849-90

14	1524.5	38.3	787	14	US-10-227-873-90	Sequence 90, Appl
15	1524.5	38.3	787	14	US-10-227-883-90	Sequence 90, Appl
16	1524.5	38.3	787	14	US-10-219-076-90	Sequence 90, Appl
17	1524.5	38.3	787	14	US-10-230-434-90	Sequence 90, Appl
18	1524.5	38.3	787	14	US-10-219-003-90	Sequence 90, Appl
19	1524.5	38.3	787	14	US-10-219-075-90	Sequence 90, Appl
20	1524.5	38.3	787	14	US-10-219-464-90	Sequence 90, Appl
21	1524.5	38.3	787	14	US-10-219-466-90	Sequence 90, Appl
22	1524.5	38.3	787	14	US-10-219-479-90	Sequence 90, Appl
23	1524.5	38.3	787	14	US-10-219-481-90	Sequence 90, Appl
24	1524.5	38.3	787	14	US-10-230-260-90	Sequence 90, Appl
25	1524.5	38.3	787	14	US-10-232-231-90	Sequence 90, Appl
26	1524.5	38.3	787	14	US-10-232-233-90	Sequence 90, Appl
27	1524.5	38.3	787	14	US-10-218-165-90	Sequence 90, Appl
28	1524.5	38.3	787	14	US-10-218-956-90	Sequence 90, Appl
29	1524.5	38.3	787	14	US-10-219-468-90	Sequence 90, Appl
30	1524.5	38.3	787	14	US-10-219-478-90	Sequence 90, Appl
31	1524.5	38.3	787	14	US-10-219-536-90	Sequence 90, Appl
32	1524.5	38.3	787	14	US-10-233-205-90	Sequence 90, Appl
33	1524.5	38.3	787	14	US-10-219-072-90	Sequence 90, Appl
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45	1524.5	38.3	787	14	US-10-232-229-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1

US-10-054-683-19
; Sequence 19, Application US/10054683
; Publication No. US20030044813A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Cancer-Testis Antigens
; FILE REFERENCE: L0461/7125 (JRV)
; CURRENT APPLICATION NUMBER: US/10/054,683
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/280,718
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/285,154
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/327,432
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-054-683-19

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Best Local Similarity	100.0%	Pred. No. 3.5e-311		
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			0	Gaps
			0	
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Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNVYGATFOGKMCNDANTAGGVVLPRT 300
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Db 361 FISKQKSQCLHNQPRLDPPFKQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
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RESULT 2

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US-10-205-823-10
; Sequence 10, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR FILING DATE: 2001-07-25
; PRIOR FILING DATE: 2001-07-25
; PRIOR FILING DATE: 2001-07-25
; PRIOR FILING DATE: 2001-08-22
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; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-205-823-10
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Best Local Similarity 100.0%; Pred. No. 3,5e-311;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MWVLFLLSLGGLRMDSNFDSLPVQITVPKIRSIIEGIESQASYKIVIEGKPYTVNLM 60
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Db 61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE 120
QY 121 NVSYGTEPLESSVGFHVIVQVHKHKKADVSLYNEKDIESRDLSPKLSAEPQODFAKYIE 180
Db 121 NVSYGTEPLESSVGFHVIVQVHKHKKADVSLYNEKDIESRDLSPKLSAEPQODFAKYIE 180
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Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNVYGATFOGKMCNDANTAGGVVLPRT 300
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Db 301 ISLESIAVILAOQLLSLGMGTYDDINKCQCAGVACIMNPEAIHPSGVKIFSNCSFEDFAH 360
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US-10-473-603-19

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; Sequence 19, Application US/10473603
; Publication No. US20040235066A1
; GENERAL INFORMATION:
; APPLICANT: SCANLAN, Matthew
; APPLICANT: CHEN, Yao-Tseng
; TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
; FILE REFERENCE: L0461.701550S00
; CURRENT FILING DATE: 2003-09-30
; PRIOR FILING DATE: 2003-03-29
; PRIOR APPLICATION NUMBER: PCT/US02/09808
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 10/054,683
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/280,718
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/285,154
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/327,432
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 734
; TYPE: PR1
; ORGANISM: Homo Sapiens
US-10-473-603-19

Query Match      100.0%; Score 3984; DB 17; Length 734;
Best Local Similarity 100.0%; Pred. No. 3.5e-311;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWVFLSLGLGRLMDSNFDSPVQITVPEKIRSIIEGIESQASQYKIVIEGKPYTVNL 60
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DB 181 MHVIVEKQLYNHMGSDTTVVAQVQFOLIGLTNAIFVSFNITIIISLLEWIDENKIATTG 240
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DB 241 EANELLHTFLRWKTSYLVRPHDVAFLVYREKSNVYGATFQGMKCDANYAGGVVLHPRT 300
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QY 361 FISKQKSOCLHNPRLDPPFPKQAVCGNAKLEAGECDCCGTEQDCALIGTCCDIATCRF 420
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DB 481 WICIDGVCMSGDKOCTDTTPEKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTCEADNLQ 540
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DB 601 RNQRCSVSSYGLDYCTTDCNDRGVNCKKCHCSASYLPPDCSVQSDLWPGGSIDSGNF 660

; Sequence 19, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 735
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-205-823-8

Query Match      99.6%; Score 3969.5; DB 14; Length 735;
Best Local Similarity 99.7%; Pred. No. 5.1e-310;
Matches 733; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MW-VLFLSLGLGRLMDSNFDSPVQITVPEKIRSIIEGIESQASQYKIVIEGKPYTVNL 59
DB 1 MWVFLSLGLGRLMDSNFDSPVQITVPEKIRSIIEGIESQASQYKIVIEGKPYTVNL 60
QY 60 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLQF 119
DB 61 MQKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLQF 120
QY 120 ENVSYGIEPLESSVGFHVYQVKKKADVSLYNEKDIESRDLSPKLOSAPQODFAKYI 179
DB 121 ENVSYGIEPLESSVGFHVYQVKKKADVSLYNEKDIESRDLSPKLOSAPQODFAKYI 180
QY 180 EMHVIYVEKQLYNHMGSDTTVVAQVQFOLIGLTNAIFVSFNITIIISLLEWIDENKIATT 239
DB 181 EMHVIYVEKQLYNHMGSDTTVVAQVQFOLIGLTNAIFVSFNITIIISLLEWIDENKIATT 240
QY 240 GEANELLHTFLRWKTSYLVRPHDVAFLVYREKSNVYGATFQGMKCDANYAGGVVLHPR 299
DB 240 GEANELLHTFLRWKTSYLVRPHDVAFLVYREKSNVYGATFQGMKCDANYAGGVVLHPR 299
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Db 241 GEANELLHFLRWKTSYLVLRPHDVAFLLYVREKSNVVGATFGKMCNDANYAGGVVLR 300
QY 300 TISLESIAVLAQLLSMGITVDDINKKOCGSAVCIIMNPEAIHFGVKIFSNCSFEDFA 359
Db 301 TISLESIAVLAQLLSMGITVDDINKKOCGSAVCIIMNPEAIHFGVKIFSNCSFEDFA 360
QY 360 HFTSKOKSOCLHNPRLDPFKQAVCGNAKLEAGEBCDGTRODCALIGETCCDIATCR 419
Db 361 HFTSKOKSOCLHNPRLDPFKQAVCGNAKLEAGEBCDGTRODCALIGETCCDIATCR 420
QY 420 FKAGSNCAEGPCCECLFMSKERMCRPSFECDLPEYCNCGSSASCSPENHYVQTGHPCGLN 479
Db 421 FKAGSNCAEGPCCECLFMSKERMCRPSFECDLPEYCNCGSSASCSPENHYVQTGHPCGLN 480
QY 480 QWICIDGVCMSGDKQCTDTFGKEVEFGPSPCYSHLNSKTDVSGNCGISDSGYTQCEADNL 539
Db 481 QWICIDGVCMSGDKQCTDTFGKEVEFGPSPCYSHLNSKTDVSGNCGISDSGYTQCEADNL 540
QY 540 QCGKLICKYVKGFLQIPRATIIYANISGHLCTAVEFASDHADSQKWIKDGTSCGSKNV 599
Db 541 QCGKLICKYVKGFLQIPRATIIYANISGHLCTAVEFASDHADSQKWIKDGTSCGSKNV 600
QY 600 CRNQRVCSSYLGVDCTTDCNDRGVCCNKKHCHCSASYLPDPCSVOQSDLWPGGSDSGN 659
Db 601 CRNQRVCSSYLGVDCTTDCNDRGVCCNKKHCHCSASYLPDPCSVOQSDLWPGGSDSGN 660
QY 660 FPPVAIPARIPERRIENIYHSPKMRWPFLLFPFFIIFCVLTAIMVKVNFQKRWRTED 719
Db 661 FPPVAIPARIPERRIENIYHSPKMRWPFLLFPFFIIFCVLTAIMVKVNFQKRWRTED 720
QY 720 YSSDEQSESEPKG 734
Db 721 YSSDEQSESEPKG 735

RESULT 5

US-10-205-823-6
; Sequence 6, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 753
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-205-823-6
Query Match 97.8%; Score 3898; DB 14; Length 753;
Best Local Similarity 99.0%; Pred. No. 2.9e-304;
Matches 718; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 10 LGGLRMDSNFSLPQVITVPEKIRSIIEGIESQASYKIVIEGKPYTNLMQKNFLPHNF 69
Db 29 LGKLYTDQDFSLPAQITVPEKIRSIIEGIESQASYKIVIEGKPYTNLMQKNFLPHNF 88
QY 70 RYVSYSGTGMKPLDODFONFCHYQYIBGYPKSVVMSTCTGLRGVLOFENVSYGIEPL 129
Db 89 RYVSYSGTGMKPLDODFONFCHYQYIBGYPKSVVMSTCTGLRGVLOFENVSYGIEPL 148
QY 130 ESSVGFPEHVIYQVKKKADVLYNEKDIERSDLSPKLSAEQQDFQAKIEMHVI VEKQL 189
Db 149 ESSVGFPEHVIYQVKKKADVLYNEKDIERSDLSPKLSAEQQDFQAKIEMHVI VEKQL 208
QY 190 YNHMGSDTTTVAQKVFQGLIGNAIFVSNITIIILSSLELWIDENKIATGGEANELLHTF 249
Db 209 YNHMGSDTTTVAQKVFQGLIGNAIFVSNITIIILSSLELWIDENKIATGGEANELLHTF 268
QY 250 LRWKTSLVLRPHDVAFLLYVREKSNYVCATFGKMCNDANYAGGVVLRPTTISLESIAVI 309
Db 269 LRWKTSLVLRPHDVAFLLYVREKSNYVCATFGKMCNDANYAGGVVLRPTTISLESIAVI 328
QY 310 LAQLLSLSMGITVDDINKKOCGSAVCIIMNPEAIHFGSVKIFSNCSFEDFAHFTSKOKSQ 369
Db 329 LAQLLSLSMGITVDDINKKOCGSAVCIIMNPEAIHFGSVKIFSNCSFEDFAHFTSKOKSQ 388
QY 370 LHNQPRLDPPFKQAVCGNAKLEAGEBCDGTQDCALIGETCCDIATCRFKAGSNCAEG 429
Db 389 LHNQPRLDPPFKQAVCGNAKLEAGEBCDGTQDCALIGETCCDIATCRFKAGSNCAEG 448
QY 430 PCCECLFMSKERMCRPSFECDLPEYCNCGSSASCSPENHYVQTGHPCGLNQCICDGVCM 489
Db 449 PCCECLFMSKERMCRPSFECDLPEYCNCGSSASCSPENHYVQTGHPCGLNQCICDGVCM 508
QY 490 SGDQKQCTDTFGKEVEFGPSPCYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICKYV 549
Db 509 SGDQKQCTDTFGKEVEFGPSPCYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICKYV 568
QY 550 GKFLQIPRATIIYANISGHLCTAVEFASDHADSQKWIKDGTSCGSKNVCRNQRVCSS 609
Db 569 GKFLQIPRATIIYANISGHLCTAVEFASDHADSQKWIKDGTSCGSKNVCRNQRVCSS 628
QY 610 YLGYDCTTDCNDRGVCCNKKHCHCSASYLPDPCSVOQSDLWPGGSDSGNPPVAIPARL 669
Db 629 YLGYDCTTDCNDRGVCCNKKHCHCSASYLPDPCSVOQSDLWPGGSDSGNPPVAIPARL 688
QY 670 PERRYENIYHSPKMRWPFLLFPFFIIFCVLTAIMVKVNFQKRWRTEDYSSDEQPESE 729
Db 689 PERRYENIYHSPKMRWPFLLFPFFIIFCVLTAIMVKVNFQKRWRTEDYSSDEQPESE 748
QY 730 SEPKG 734
Db 749 SEPKG 753

RESULT 6

US-10-227-884-90
; Sequence 90, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C79
CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
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PRIOR FILING DATE: 1999-03-19
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PRIOR FILING DATE: 1999-03-23
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; PRIOR APPLICATION NUMBER: 60/082804
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; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
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; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      38.3%; Score 1524.5; DB 14; Length 787;
Best Local Similarity 41.1%; Pred. No. 2.1e-113;
Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18;

QY 1 MWVLFLLSGGLRMD-SNFDLSPVQITVPEKIRSIIEGIE---SQASYKIVIEGKPYT 56
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 LWL--LLAGLCGLASRPGFQNSLLQIVPEKIQTNDSEIEYEQISYIIPIDEKLYT 61

QY 57 VNLMOKNFLPHNPRVYSYSGTGIMKPLDQDFQNFCHYQGYEGYKPSVVMVSTCTGLRGV 116
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VHLKQRYFLADNFMILYN-QGSMNTYSSDIQTQCYQGNIEGYPSDMSVTLSTCSGLRGI 120

QY 117 LQFENVSYGIEPLESSVGFHEHYQVKKHKKADVSLYNEKDIESR---DLSPKLSQAEPPQ 173
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 LQFENVSYGIEPLESSVGFHEHYQVKKHKKADVSLYNEKDIESR---DLSPKLSQAEPPQ 180

QY 174 D--FAXIEMHVIVEKQLYNHMGSDTTVAQKVFQILGTNAIFVSFNITILSSLELWI 231
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 PDLFPLYLEHMHVVDKTYDYGSDMSVITNKVIEIVGLANSMTQPKVTIVLSSLELWS 240

QY 232 DENKIATTEGABELLHTFLRWKTSYLVLRPHDVAFLVREKSNYVGGATQGGKCDANYA 291
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 DENKISTVGEADQLQKFLWKQSYLNLPRHDIAYLLIYMDYPRYLGAVPFGTMCITRYS 300

QY 292 GGVVLPRTISLESIAVILAQLLSMGITYDDINKQCCSGAVCIMNPEAHFSGVKIFS 351
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 AGVALYPKETLEAFVIVTQMLALSIGSYDDPKKQCCSESTCIMNPEVQSNVGVKTF 360

QY 352 NCSFEDFAHRTSKOSCLHNPRLDFFFOQAVCGNAKLEAGEECDCGTEDCALIGET 411
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 SCSLRSFQNFISNVGVKCLQNKPMQK-KSPKPVCGNRLGNEICDCGTEAQCG--PAS 417

QY 412 CDDIATCRFKAGSNCAEGPCENCLFMSKERMCRP-SFECDLPEYCNCGSSASCPENHYV 470
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
418 CDFRTVLVDGAKYKGLCKCQQLIQSGVECHRPKAHPECDIAENCNGSSPCEGPDITL 477

QY 471 QTHPCGLNQCWICIDGVCMSGDQCTDTFGKEVEFGPSECVSHLNSKTDVSGNCGIS-DS 529
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
478 INGLSCKNNKFCVDGDCHLDARCESVFGKGSRNAPFACVEEQSQSDRFGNCGDRNN 537

QY 530 GYTQCEADNLQCKLKICYKGFLLQIPRATIIYANISGHLCTIAVEFASDHASQRMWIK 589
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
538 KYVFCGWRNLICGLRVCTYPRKPFHOENGSDVIYAFVDSVCITVDYKLPRTVPDPLAVK 597

QY 590 DGTSCGSKNYCRNORCVSSYL---GYDCTTDKNDRGVGNCKKHCHCSASYLPDPCSVQ 646
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
598 NGSQCDIGRVNRECVESRIIICASAVC-SQQSCGHGVCDNRKCHCSGYPKPNQIR 656

QY 647 SLDLPGGSI---DSGNFPFVPAIPARLPERRYIENIYHSPMRW--PFFLIPFFIIFCV 700
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
657 S---KGFSIFPEEDMGSI-----MERASGKTENTWLLGLIALPILIV---696

QY 701 LIAIMVKNVQRKWRTEYSSDEQPESEPKG 734
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
697 -TTAIVLARKQLKKWFAKE---EFPPSSSEKSEG 726
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RESULT 8

US-10-230-338-90

; Sequence 90, Application US/10230338

; Publication No. US20030044934A1

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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 90
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-230-338-90

Query Match      38.3%; Score 1524.5; DB 14; Length 787;
Best Local Similarity 41.1%; Pred. No. 2.1e-113;
Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18;

QY 1 MWVLFLLSGGLRMD-SNFDLSPVQITVPEKIRSIIEGIE---SQASYKIVIEGKPYT 56
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 LWL--LLAGLCGLASRPGFQNSLLQIVPEKIQTNDSEIEYEQISYIIPIDEKLYT 61

QY 57 VNLMOKNFLPHNPRVYSYSGTGIMKPLDQDFQNFCHYQGYEGYKPSVVMVSTCTGLRGV 116
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VHLKQRYFLADNFMILYN-QGSMNTYSSDIQTQCYQGNIEGYPSDMSVTLSTCSGLRGI 120

QY 117 LQFENVSYGIEPLESSVGFHEHYQVKKHKKADVSLYNEKDIESR---DLSPKLSQAEPPQ 173
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 LQFENVSYGIEPLESSVGFHEHYQVKKHKKADVSLYNEKDIESR---DLSPKLSQAEPPQ 180

QY 174 D--FAXIEMHVIVEKQLYNHMGSDTTVAQKVFQILGTNAIFVSFNITILSSLELWI 231
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 PDLFPLYLEHMHVVDKTYDYGSDMSVITNKVIEIVGLANSMTQPKVTIVLSSLELWS 240

QY 232 DENKIATTEGABELLHTFLRWKTSYLVLRPHDVAFLVREKSNYVGGATQGGKCDANYA 291
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 DENKISTVGEADQLQKFLWKQSYLNLPRHDIAYLLIYMDYPRYLGAVPFGTMCITRYS 300

QY 292 GGVVLPRTISLESIAVILAQLLSMGITYDDINKQCCSGAVCIMNPEAHFSGVKIFS 351
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 AGVALYPKETLEAFVIVTQMLALSIGSYDDPKKQCCSESTCIMNPEVQSNVGVKTF 360
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QY 352 NCSFEDFAHFISKQSOCLHNQRLDPFFKQAVCGNAKLEAGBECDCGTEQDCALIGET 411
Db 361 SCSLSRFQFISNVGVKCLQNKQPMQK-KSPKPVCGNRLGEGNEICDCGTEAQCG--PAS 417
QY 412 CCDIATCRFKAGSNCAEGPCENCLFMSKERMCRP-SFEECDLPEYCNCGSSASCPENHYV 470
Db 418 CDFRFTCVLKGAKCYKGLCKQCQILQSGVECRKPAHPCDIAENCGSSPECGPDITL 477
QY 471 QTGHPCGLNQMICIDGCMGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529
Db 478 INGLSKNNKFCICVDGDCHDLARCESVFGKSRNAPFACYEBIQSDRFGNCGRDRNN 537
QY 530 GYTQCEADNLQCKLICKYVGFELLQIPRATIIYANISGHLCTIAVEFASDHASQKWK 589
Db 538 KYVFCGWRNLICGRLVCTYPTRKPFHQENGVDVIAFVRDSVCITVDYKLPRTVPDPLAVK 597
QY 590 DGTSGSNKVCNRCNORCVSSSYL---GYDCTTKCNDRGVGNCKKHCHCSASYLPDQCSVQ 646
Db 598 NGSQCDIGRVCNRECVESRIIKASAHVC-SQCSGSHGVCDNRNCKCHCSGYKPPNCOIR 656
QY 647 SLDWPGGSI-----DSGNFPFPAIPARLPERRYIENIYHSPMRW--PFFLFIFFIFCV 700
Db 657 S---KGFSIFPEEDMGSI-----MERASGKTENTWLLGFLIALPILIV--- 696
QY 701 LIAIMVKVNFORKKWRTEYSSDEQPESESEPKG 734
Db 697 -TTAIVLARKQLKWKFAKE---EEFSSSEKSEG 726

RESULT 9
US-10-218-631-90
; Sequence 90, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1G14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 90
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; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-90

Query Match      38.3%; Score 1524.5; DB 14; Length 787;
Best Local Similarity 41.4%; Pred. No. 2.1e-113;
Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18;

QY 1 MWVLLSGLGGIRMD-SNFDSLPVQITVPEKIRSIKEGIE---SQASYKIVIEGPKYT 56
Db 4 LML--LLAGLCGLLASRPGFQNSLLQIVPEKIQTNWDSSEIEYEISIIPIDEKLYT 61
QY 57 VNLQKNFUPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGURGV 116
Db 62 VHLKQRYFLADNFMILYN-QGSMNTYSSDIQTCYQYQYQYQYQYQYQYQYQYQYQY 120
QY 117 LQFENYSGIEPLESSVGFHEHVIYQVKKKADVSLYNEKDIESR---DLSEFKLOSAPQ 173
Db 121 LQFENYSGIEPLESAVEFQHVLYLKUNEDNDIAIFIDRSLEKQPMDDNIFISEKSEPAV 180
QY 174 D--FAKYIEHVIYVEKQLYNHNMGSDTTVVAQFQFQIQLTNAIFVSFNITIISSLSLWI 231
Db 181 PDLFPLYLEHVIYVDKTLIDYWGSDSMIVTNKVIIEIVGLANSMTQFKVTIVLSLSLWS 240
QY 232 DENKIATGEANBLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVYGATFGKMKCDANYA 291
Db 241 DENKISTVGEADLLQKFLWKQSYLNLPHDIAYLIIYMDYPRYLGAVPFGTMCITRYS 300
QY 292 GGVVHLPRITLESILAVILAQLLSMGITYDDINKCQSGAVCINMPEAIHPSGVKIFS 351
Db 301 AGVALYPEKITELEAFVITQMLALSLGISYDDPKKQCSSESTCINMPEVYVQSNKVTF 360
QY 352 NCSFEDFAHFISKQSOCLHNQRLDPFFKQAVCGNAKLEAGBECDCGTEQDCALIGET 411
Db 361 SCSLSRFQFISNVGVKCLQNKQPMQK-KSPKPVCGNRLGEGNEICDCGTEAQCG--PAS 417
QY 412 CCDIATCRFKAGSNCAEGPCENCLFMSKERMCRP-SFEECDLPEYCNCGSSASCPENHYV 470
Db 418 CDFRFTCVLKGAKCYKGLCKQCQILQSGVECRKPAHPCDIAENCGSSPECGPDITL 477
QY 471 QTGHPCGLNQMICIDGCMGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529
Db 478 INGLSKNNKFCICVDGDCHDLARCESVFGKSRNAPFACYEBIQSDRFGNCGRDRNN 537
QY 530 GYTQCEADNLQCKLICKYVGFELLQIPRATIIYANISGHLCTIAVEFASDHASQKWK 589
Db 538 KYVFCGWRNLICGRLVCTYPTRKPFHQENGVDVIAFVRDSVCITVDYKLPRTVPDPLAVK 597
QY 590 DGTSGSNKVCNRCNORCVSSSYL---GYDCTTKCNDRGVGNCKKHCHCSASYLPDQCSVQ 646
Db 598 NGSQCDIGRVCNRECVESRIIKASAHVC-SQCSGSHGVCDNRNCKCHCSGYKPPNCOIR 656
QY 647 SLDWPGGSI-----DSGNFPFPAIPARLPERRYIENIYHSPMRW--PFFLFIFFIFCV 700
Db 657 S---KGFSIFPEEDMGSI-----MERASGKTENTWLLGFLIALPILIV--- 696
QY 701 LIAIMVKVNFORKKWRTEYSSDEQPESESEPKG 734
Db 697 -TTAIVLARKQLKWKFAKE---EEFSSSEKSEG 726

RESULT 10
US-10-230-414-90
; Sequence 90, Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
```



```

Db      538 KYVFCGWRNLICGRVLVCTYPTRKPHQENGNDVVIYAFVRDSCVITVDYKULPRTVDPDLAVK 599
Qy      590 DGTSCGNKVCNRNCVSSSYL---GYDCTTDKNDRGVCNNKXGCHCSASYLPPDCSVQ 646
Db      598 NGSQCDIGRVCNRCVESRIIKASAHVC-SQCCSGHGVCDSENKCHCSPGYKPCNQIR 656
Qy      647 SDLWPGSSI-----DSGNPPPPVAIPARLPERRRYENIYHSKPNRW--PPPLFIPTPIIFCV 700
Db      657 S---KGFSIPPEEDMGSI-----MERASGKTENTWLLGLFLIALPILIV---696
Qy      701 LIAIMVKVNFQKKWRTEYDSSDEQESSEPKG 734
Db      697 -TTAIVLARKQLKKWFAKE---EPPPSSEKSEG 726

RESULT 13
US-10-218-849-90
; Sequence 90, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deanovers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 245
; SEQ ID NO 90
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-90

Query Match      38.3%; Score 1524.5; DB 14; Length 787;
Best Local Similarity 41.1%; Pred.No.2.1e-113;
Matches 310; Conservative 134; Mismatches 259; Indels 51; Gaps 18

Qy      1 MWLFLSLGGLRMD-SNFDSLPQVITVPEKIRSIIEGIE---SQASYKIVIEGKPYT 56
Db      4 LWL--LLAGLGLLASRPGFQNSLLQIVPEKIQTNDSSIEIEVEQIYSIIPIDEKLYT 61
Qy      57 VNLQKNFLPHNFRVYSGTGIMKPLDQDFQNFCHYOGYIEGYPKSVVMVSTCTGLRGV 116
Db      62 VHLKQRYFLADNFMFMYLYN-QGSNMNTYSSDIQTQCYQCNIEGYPDSVWTLSTCSGLRGI 120
Qy      117 LQFNVSNGTIEPLESSGFEHVIYQVHKHKAADVSLYNEKDIESR---DLSEKLQSAEPQQ 173
Db      121 LQFNVSNGTIEPLESAGEFQFVLYLKRKNEDNDIAIFIDRLSKBQPMDDNIFISEKSEPAV 180
Qy      174 D--PAKTIEMHVIYEKQLYNHNMGSDTTVVAQKVFOLIGLTNAIFVSFNITILSLELWI 231
Db      181 PDLFPLYLEMHIVDKTLYDWGSDSMVTNKNVIEIVGLANSMTQFKVTVILSLELWS 240
Qy      232 DENKIATTEANELLHTFTLRWKTYSVLVLRPHDVAFLLYVREKSNVYGATFGQKMDANYA 291
Db      241 DENKISTVGEADELLQKPLEWKQSYNLNRPHDIAVLLIYMDYPRYLGVAFPGTMCITRYS 300
Qy      292 GGVLHPRTISLESIAVTLAQILSLSMGITYDDINKKCCSGAVCTMNPETHFSGVKIES 351
Db      301 AGVALYKREITLEPAFVITVQMLALSLSGISYDDPKKCCQCSSESTCIIMNFEVQNSGKVTFS 360
Qy      352 NCSPEDFAHFITSKOKSCLHNOPRLDPFFKQAVCGNAKLRAAGESCDGTCGEOCDALIGET 411

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1	1	PRIOR FILING DATE: 1998-09-24	
2	2	PRIOR APPLICATION NUMBER: 60/101922	
3	3	PRIOR FILING DATE: 1998-09-24	
4	4	PRIOR APPLICATION NUMBER: 60/106178	
5	5	PRIOR FILING DATE: 1998-10-28	
6	6	PRIOR APPLICATION NUMBER: 60/106248	
7	7	PRIOR FILING DATE: 1998-10-29	
8	8	PRIOR APPLICATION NUMBER: 60/106464	
9	9	PRIOR FILING DATE: 1998-10-30	
10	10	PRIOR APPLICATION NUMBER: 60/106905	
11	11	PRIOR FILING DATE: 1998-11-03	
12	12	PRIOR APPLICATION NUMBER: 60/108787	
13	13	PRIOR FILING DATE: 1998-11-17	
14	14	PRIOR APPLICATION NUMBER: 60/108801	
15	15	PRIOR FILING DATE: 1998-11-17	
16	16	PRIOR APPLICATION NUMBER: 60/108849	
17	17	PRIOR FILING DATE: 1998-11-18	
18	18	PRIOR APPLICATION NUMBER: 60/112422	
19	19	PRIOR FILING DATE: 1998-12-15	
20	20	PRIOR APPLICATION NUMBER: 60/113296	
21	21	PRIOR FILING DATE: 1998-12-22	
22	22	PRIOR APPLICATION NUMBER: 60/113605	
23	23	PRIOR FILING DATE: 1998-12-23	
24	24	PRIOR APPLICATION NUMBER: 60/113621	
25	25	PRIOR FILING DATE: 1998-12-23	
26	26	PRIOR APPLICATION NUMBER: 60/115558	
27	27	PRIOR FILING DATE: 1999-01-12	
28	28	PRIOR APPLICATION NUMBER: 60/115565	
29	29	PRIOR FILING DATE: 1999-01-12	
30	30	PRIOR APPLICATION NUMBER: 60/115733	
31	31	PRIOR FILING DATE: 1999-01-12	
32	32	PRIOR APPLICATION NUMBER: 60/119549	
33	33	PRIOR FILING DATE: 1999-02-10	
34	34	PRIOR APPLICATION NUMBER: 60/123618	
35	35	PRIOR FILING DATE: 1999-03-10	
36	36	PRIOR APPLICATION NUMBER: 60/125259	
37	37	PRIOR FILING DATE: 1999-03-19	
38	38	PRIOR APPLICATION NUMBER: 60/125775	
39	39	PRIOR FILING DATE: 1999-03-23	
40	40	PRIOR APPLICATION NUMBER: 60/126773	
41	41	PRIOR FILING DATE: 1999-03-29	
42	42	PRIOR APPLICATION NUMBER: 60/127887	
43	43	PRIOR FILING DATE: 1999-04-05	
44	44	PRIOR APPLICATION NUMBER: 60/130232	
45	45	PRIOR FILING DATE: 1999-04-21	
46	46	PRIOR APPLICATION NUMBER: 60/131022	
47	47	PRIOR FILING DATE: 1999-04-26	
48	48	PRIOR APPLICATION NUMBER: 60/131270	
49	49	PRIOR FILING DATE: 1999-04-27	
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51	51	PRIOR FILING DATE: 1999-04-27	
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53	53	PRIOR FILING DATE: 1999-04-28	
54	54	PRIOR APPLICATION NUMBER: 60/134287	
55	55	PRIOR FILING DATE: 1999-05-14	
56	56	PRIOR APPLICATION NUMBER: 60/140650	
57	57	PRIOR FILING DATE: 1999-06-22	
58	58	PRIOR APPLICATION NUMBER: 60/140723	
59	59	PRIOR FILING DATE: 1999-08-22	
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61	61	PRIOR FILING DATE: 1999-06-23	
62	62	PRIOR APPLICATION NUMBER: 60/144758	
63	63	PRIOR FILING DATE: 1999-07-20	
64	64	PRIOR APPLICATION NUMBER: 60/145698	
65	65	PRIOR FILING DATE: 1999-07-26	
66	66	PRIOR APPLICATION NUMBER: 60/146222	
67	67	PRIOR FILING DATE: 1999-07-28	
68	68	PRIOR APPLICATION NUMBER: 60/146963	
69	69	PRIOR FILING DATE: 1999-08-03	
70	70	PRIOR APPLICATION NUMBER: 60/149320	
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72	72	PRIOR APPLICATION NUMBER: 60/149638	
73	73	PRIOR FILING DATE: 1999-08-17	

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PRIOR FILING DATE:	1998-08-11
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PRIOR APPLICATION NUMBER:	60/099596
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099598
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PRIOR APPLICATION NUMBER:	60/099812
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PRIOR APPLICATION NUMBER:	60/099816
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PRIOR APPLICATION NUMBER:	60/100038
PRIOR FILING DATE:	1998-09-11
PRIOR APPLICATION NUMBER:	60/100385
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PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100848
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PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/101477
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101738
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101741
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101786
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PRIOR APPLICATION NUMBER:	60/106178
PRIOR FILING DATE:	1998-10-28
PRIOR APPLICATION NUMBER:	60/106248
PRIOR FILING DATE:	1998-10-29
PRIOR APPLICATION NUMBER:	60/106464
PRIOR FILING DATE:	1998-10-30
PRIOR APPLICATION NUMBER:	60/106905
PRIOR FILING DATE:	1998-11-03
PRIOR APPLICATION NUMBER:	60/108787
PRIOR FILING DATE:	1998-11-17
PRIOR APPLICATION NUMBER:	60/108801
PRIOR FILING DATE:	1998-11-17
PRIOR APPLICATION NUMBER:	60/108849
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PRIOR APPLICATION NUMBER:	60/112422
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PRIOR APPLICATION NUMBER:	60/113621
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PRIOR FILING DATE:	1999-01-12
PRIOR APPLICATION NUMBER:	60/115565
PRIOR FILING DATE:	1999-01-12
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PRIOR FILING DATE:	1999-01-12
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;	PRIOR FILING DATE:	1999-02-10	
;	PRIOR APPLICATION NUMBER:	60/123618	
;	PRIOR FILING DATE:	1999-03-10	
;	PRIOR APPLICATION NUMBER:	60/125259	
;	PRIOR FILING DATE:	1999-03-19	
;	PRIOR APPLICATION NUMBER:	60/125775	
;	PRIOR FILING DATE:	1999-03-23	
;	PRIOR APPLICATION NUMBER:	60/126773	
;	PRIOR FILING DATE:	1999-03-29	
;	PRIOR APPLICATION NUMBER:	60/127887	
;	PRIOR FILING DATE:	1999-04-05	
;	PRIOR APPLICATION NUMBER:	60/130232	
;	PRIOR FILING DATE:	1999-04-21	
;	PRIOR APPLICATION NUMBER:	60/131022	
;	PRIOR FILING DATE:	1999-04-26	
;	PRIOR APPLICATION NUMBER:	60/131270	
;	PRIOR FILING DATE:	1999-04-27	
;	PRIOR APPLICATION NUMBER:	60/131291	
;	PRIOR FILING DATE:	1999-04-27	
;	PRIOR APPLICATION NUMBER:	60/131445	
;	PRIOR FILING DATE:	1999-04-28	
;	PRIOR APPLICATION NUMBER:	60/134287	
;	PRIOR FILING DATE:	1999-05-14	
;	PRIOR APPLICATION NUMBER:	60/140650	
;	PRIOR FILING DATE:	1999-05-22	
;	PRIOR APPLICATION NUMBER:	60/140723	
;	PRIOR FILING DATE:	1999-06-22	
;	PRIOR APPLICATION NUMBER:	60/141037	
;	PRIOR FILING DATE:	1999-06-23	
;	PRIOR APPLICATION NUMBER:	60/144758	
;	PRIOR FILING DATE:	1999-07-20	
;	PRIOR APPLICATION NUMBER:	60/145698	
;	PRIOR FILING DATE:	1999-07-26	
;	PRIOR APPLICATION NUMBER:	60/146222	
;	PRIOR FILING DATE:	1999-07-28	
;	PRIOR APPLICATION NUMBER:	60/146963	
;	PRIOR FILING DATE:	1999-08-03	
;	PRIOR APPLICATION NUMBER:	60/151733	
;	PRIOR FILING DATE:	1999-08-31	
;	PRIOR APPLICATION NUMBER:	60/149320	
;	PRIOR FILING DATE:	1999-08-17	
;	PRIOR APPLICATION NUMBER:	60/149638	
;	PRIOR FILING DATE:	1999-08-17	
;	PRIOR APPLICATION NUMBER:	60/151733	
;	PRIOR FILING DATE:	1999-08-31	
;	PRIOR APPLICATION NUMBER:	60/164418	
;	PRIOR FILING DATE:	1999-11-09	
;	PRIOR APPLICATION NUMBER:	60/166361	
;	PRIOR FILING DATE:	1999-11-16	
;	PRIOR APPLICATION NUMBER:	60/169445	
;	PRIOR FILING DATE:	1999-12-07	
;	PRIOR APPLICATION NUMBER:	60/169495	
;	PRIOR FILING DATE:	1999-12-07	
;	PRIOR APPLICATION NUMBER:	60/169835	

Query Match	38.3%	Score 1524.5;	DB 14;	Length 787;
Best Local Similarity	41.1%;	Pred. No. 2.1e-113;		
Matches	310;	Conservative 134;	Mismatches 259;	Indels 51; Gaps 18;
Qy	1	MWLFLLSLGLGGRMD--SNFDSLUPVQITVPEKRSIIKEGIE--SQASKYKIVIEGPKYT	56	
Db	4	LWL--LLAGLGLASRPGFNSLLQIVPEKLTQTNDSSEIEYEQISVIIPIDEKLYT	61	
Qy	57	VNLMQKNFPLPHNPRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVNMVSTCTGLRGV	116	
Db	62	VHLKQRYFLADNFMIIYLN--QGSMTYSSDIQTQCYQGNIEGYPDSMVLSTCSTGLRGI	120	
Qy	117	LQFENYSYGIETPLESSGPEHVITYOVGHKADVSLVNEKDIERS--DLGFKLQSAEPQ	173	
Db	121	LQFENYSYGIETPLESAVEFQHVLYKLQNDNDTAIFDRSLKEQPMDDNFISEKSEPAV	180	
Qy	174	D--FAXYIEMHVIVEKOLYNHMGSDTTVAQKVFQIIGLTNAIFVSNFIITILSSLELWI	231	
Db	181	PDLFPLYLENHIIVVDKTLVDYMGSDSMIVTKNVEIIVGLANSNFTQPKVITVLSLELWS	240	

Qy	232	DENKIATTGEANELLHLLTFLRWKTSVVLVRPHDVAFLLVYRKSNTVGGATFGQMKCDANYA	291
Db	241	DENKISTVGEADELLQKLEWKQSYNLNRPDHIAYLLIYMDYPRYGLVFPFGTMCITRYS	300
Qy	292	GGVVLHPTITLSLAVILAQLLSLSMGITVDDINKCSCGAGVCLMNPETHFSGVKIFS	351
Db	301	AGVALYKPEITLEAFVIVTQMLALSLSGISYDDPKKCCQCSBSTCLMNPVQSGVKTFS	360
Qy	352	NCSPEDFAHFTISKQSCQLHNQRLDPFFKQOAVCGNAKLEAGEBCDCGTBODCALIGET	411
Db	361	SCSLRSFQFTSNVGVKQLONKQPQOK-KSPKPVCGNGRLEGNICDQGTAEQCG--PAS	417
Qy	412	CCDIATCRFKAGSCAEGPCCECNCLFMSKERMCRP-SPEEDCLPVYCNQSSASCENHVX	470
Db	418	CCDPRTCVLKQAKCYKGLCKQKQCILOSGVECRPKAHPCEDIAENQSSPECCPDITL	477
Qy	471	QTGHPCCGLNOMICDGVCMWSGDQCTDTFGKEVEFGFSECVSHLNSKTDVSGNCGIS-DS	529
Db	478	INGLSCKNKFICYDGDCHDLDARCESYFGKSRNAPFACYBEIOSQDRFCNGCDRNN	537
Qy	530	GYTOEADNLOCGKLIKCVKGFLLIQIPRATIIYANISGHLCIAIEFASDHADSQKWKIT	589
Db	538	KYVFCGWNLICGRILVCYPTRKPHQENGDIVIAFVDSVCLITVDYKLPRTVPDLAVK	597
Qy	590	DGTS CGSNKVCNRQCRSSSYL---GYDCTTDKNDRGVNNKHKCHCSASYLPDPDCSVQ	646
Db	598	NGSQCDIGRVCVNRCEVESRIIKASAHVC-SQCCSGHGVCDSRNKCHCSGPKYKPNQCIR	656
Qy	647	SDLWFGGSI----DSGNFPFPVAIPARLPERRVIENTIYHSPKMRW--PPFLPTFFFLIFCV	700
Db	657	S---KGFSPFPEEDMGSI-----MERASGKTENTWLLGFLIALPILIV---	696
Qy	701	LIAIMVKVNFQRKKWRTEDEYSDSEQESESPEKG	734
Db	697	-TTAIVLARKOLKKWFAXE---EEFPSSSESKEG	726

Search completed: January 10, 2005, 22:31:53
Job time : 151 secs

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OM protein - protein search, using sw model

Run on: January 10, 2005, 22:22:33 ; Search time 160 Seconds
(without alignments)
1645.671 Million cell updates/sec

Title: US-10-054-683-19
Perfect score: 734
Sequence: 1 MMVLFLLGLGLRMDNSF.....WRTDYSSDEQPSSEPKG 734

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	734	100.0	734	2	AAR87037 Human PH3
2	734	100.0	734	6	ABJ19246 Human can
3	734	100.0	734	7	ADB75186 Prostate
4	650	88.6	651	2	AAR87034 Human PH3
5	631	86.0	735	7	ADB75184 Prostate
6	609	83.0	733	7	ADB75182 Prostate
7	15	2.0	568	4	AAE10823 Human gen
8	15	2.0	668	6	ABJ26664 Human pro
9	15	2.0	759	5	AAU97037 Human LP
10	15	2.0	787	5	AAU83636 Human PRO
11	15	2.0	787	6	ABU80783 Human PRO
12	15	2.0	787	6	ABO33749 Novel hum
13	15	2.0	787	6	ABU82092 Novel hum
14	15	2.0	787	6	ABR48487 Human LAP
15	15	2.0	787	6	ABJ72272 Human PRO
16	15	2.0	787	6	ABJ72400 Human PRO
17	15	2.0	787	6	ABO34295 Human sec
18	15	2.0	787	7	ABJ72102 Human mem
19	15	2.0	787	7	ADB83580 Novel hum
20	15	2.0	787	7	ADB80686 Novel hum
21	15	2.0	787	7	ADB73227 Novel hum
22	15	2.0	787	7	ADB78309 Novel hum
23	15	2.0	787	7	ADB84957 Human PRO
24	15	2.0	787	7	ADB78063 Novel hum
25	15	2.0	787	7	ADB87129 Human PRO

26	15	2.0	787	7	ADB84711	Human PRO
27	15	2.0	787	7	ADB83826	Novel hum
28	15	2.0	787	7	ADB72981	Novel hum
29	15	2.0	787	7	ADC36819	Human PRO
30	15	2.0	787	7	ADC21809	Human PRO
31	15	2.0	787	7	ADC49840	Novel hum
32	15	2.0	787	7	ADC49039	Novel hum
33	15	2.0	787	7	ADC49556	Novel hum
34	15	2.0	787	7	ADC47417	Novel hum
35	15	2.0	787	7	ADC47162	Novel hum
36	15	2.0	787	7	ADC78037	Novel hum
37	15	2.0	787	7	ADD06272	Novel hum
38	15	2.0	787	7	ADC77791	Novel hum
39	15	2.0	787	7	ADD50754	Novel hum
40	15	2.0	787	7	ADD51000	Novel hum
41	15	2.0	787	7	ADD50481	Human PRO
42	15	2.0	787	7	ADD50235	Human PRO
43	15	2.0	787	7	ADD51246	Novel hum
44	15	2.0	787	8	ADC48793	Novel hum
45	15	2.0	787	8	ADE20964	Novel hum

ALIGNMENTS

RESULT 1
AAR87037
ID AAR87037 standard; protein; 734 AA.
XX
AC AAR87037;
XX
DT 30-SEP-1996 (first entry)
XX
DE Human PH30 beta chain sperm protein.
XX
KW Human PH30 beta chain sperm protein; contraceptive;
KW FEE integrin binding domain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 84..734
FT /note= "see AAR87035"
XX
PN WO9535118-A1.
XX
PD 28-DEC-1995.
XX
PF 06-JUN-1995; 95WO-US007295.
XX
PR 20-JUN-1994; 94US-00264101.
XX
PA (MERI) MERCK & CO INC.
XX
PI Alves K, Gupta SK, Hollis GF;
XX
DR WPI; 1996-058212/06.
XX
DR N-PSDB; AAT07328.
XX
PT Human and mouse sperm protein PH30 beta chain and related DNA - useful in
PT contraceptive vaccines.
XX
PS Example 2; Page 45-48; 85pp; English.
XX
CC Human PH30 beta chain sperm protein, having a FEE integrin binding
CC domain, is 58.9% identical to mouse and 56.5% identical to guinea pig
CC PH30 beta. The protein may be produced recombinantly and used in a
CC contraceptive composition containing an effective adjuvant and an amount
CC of sperm protein which is effective for the stimulation of antibodies
CC which bind to sperm protein in vivo, thereby preventing or substantially
XX reducing the rate of sperm-egg fusion
XX
SQ Sequence 734 AA;


```
Query Match      100.0%; Score 734; DB 2; Length 734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWVFLSLGLGGLRMDNSFSLPQVITVPEKIRSIKEGIESQASYKIVIEGKPYTVNLM 60
DB 1 MWVFLSLGLGGLRMDNSFSLPQVITVPEKIRSIKEGIESQASYKIVIEGKPYTVNLM 60
QY 61 QKNFLPHNFRVYSYSGTIGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGLVQFE 120
DB 61 QKNFLPHNFRVYSYSGTIGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGLVQFE 120
QY 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQODFAKYE 180
DB 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQODFAKYE 180
QY 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQODFAKYE 180
DB 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQODFAKYE 180
QY 181 MHVIVEKQLYNNHMGSDTTVAQKVFQGLIGNAIFVSNITIIISLSLELWIDENKIATTG 240
DB 181 MHVIVEKQLYNNHMGSDTTVAQKVFQGLIGNAIFVSNITIIISLSLELWIDENKIATTG 240
QY 241 EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGMCDANTAGGVVLHPRT 300
DB 241 EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGMCDANTAGGVVLHPRT 300
QY 301 ISLESIAVILAOQLLSLGMITYDDINKCQCSGAVCIMNPEAIHPSGVKIFSNCSFEDFAH 360
DB 301 ISLESIAVILAOQLLSLGMITYDDINKCQCSGAVCIMNPEAIHPSGVKIFSNCSFEDFAH 360
QY 361 FISKQKSOQLHNPRLDPPFPKQAVCGNAKLEAGEECDCGTEQDCALIGTCCDIATCRF 420
DB 361 FISKQKSOQLHNPRLDPPFPKQAVCGNAKLEAGEECDCGTEQDCALIGTCCDIATCRF 420
QY 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQ 480
DB 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQ 480
QY 481 WICIDGCMGDKOCTDTFGKEVEFGPSECVSHLNSKTDVSGNGCISDSGYTQCEADNLQ 540
DB 481 WICIDGCMGDKOCTDTFGKEVEFGPSECVSHLNSKTDVSGNGCISDSGYTQCEADNLQ 540
QY 541 CGKLI CKYVGFLLQI PRATIIYANISGHLICIAVEFASDHADSQKWKIDGTS CGSNKVC 600
DB 541 CGKLI CKYVGFLLQI PRATIIYANISGHLICIAVEFASDHADSQKWKIDGTS CGSNKVC 600
QY 601 RNQRCVSSYLGYDCTTDKNDRGVCNNKCHCSASVLPDSCVSQSDLPWGGSIDSGNF 660
DB 601 RNQRCVSSYLGYDCTTDKNDRGVCNNKCHCSASVLPDSCVSQSDLPWGGSIDSGNF 660
QY 661 PPVAIPARLPERRIENIYHSKPMRWPFLLFPFIIFCVLIAMVKNVQKWKRTEDY 720
DB 661 PPVAIPARLPERRIENIYHSKPMRWPFLLFPFIIFCVLIAMVKNVQKWKRTEDY 720
QY 721 SSDEQPESESEPKG 734
DB 721 SSDEQPESESEPKG 734
```

RESULT 2

```
ABJ19246
ID ABJ19246 standard; protein; 734 AA.
XX AC ABJ19246;
XX DT 28-MAR-2003 (first entry)
XX DE Human cancer/testis antigen - SEQ ID No 19.
XX KW Human; gene therapy; vaccine; cancer; cancer/testis antigen; CT antigen.
XX OS Homo sapiens.
XX PN WO200278526-A2.
```

```
XX 10-OCT-2002.
XX 29-MAR-2002; 2002WO-US009808.
XX 30-MAR-2001; 2001US-0280718P.
XX 20-APR-2001; 2001US-0285154P.
XX 05-OCT-2001; 2001US-0327432P.
XX 22-JAN-2002; 2002US-00054683.
XX (LUDW-) LUDWIG INST CANCER RES.
XX (CORR ) CORNELL RES FOUND INC.
XX Old LJ, Scanlan MJ, Chen Y;
XX WPI; 2003-040608/03.
XX N-PSDB; ABT15727.
XX Diagnosing cancer comprises contacting a biological sample isolated from
XX a subject with an agent that specifically binds to a nucleic acid
XX molecule, its expression product or fragment or an antibody that binds to
XX the product or fragment.
XX Claim 36; Page 124-126; 155pp; English.
XX The invention comprises a method for diagnosing cancer, the method
XX involves detecting the DNA or protein sequences of human cancer/testis
XX (CT) antigens that are disclosed in the invention. The method of the
XX invention is useful for detecting/diagnosing, treating and monitoring a
XX cancer or condition characterised by the expression of a human CT
XX antigen. The present amino acid sequence represents a human CT antigen of
XX the invention
XX Sequence 734 AA;
```

```
Query Match      100.0%; Score 734; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWVFLSLGLGGLRMDNSFSLPQVITVPEKIRSIKEGIESQASYKIVIEGKPYTVNLM 60
DB 1 MWVFLSLGLGGLRMDNSFSLPQVITVPEKIRSIKEGIESQASYKIVIEGKPYTVNLM 60
QY 61 QKNFLPHNFRVYSYSGTIGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGLVQFE 120
DB 61 QKNFLPHNFRVYSYSGTIGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGLVQFE 120
QY 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQODFAKYE 180
DB 121 NVSYGIEPLESSVGFHEVIYQVHKKADVSLYNEKDIESRDLSFKLOSAPQODFAKYE 180
QY 181 MHVIVEKQLYNNHMGSDTTVAQKVFQGLIGNAIFVSNITIIISLSLELWIDENKIATTG 240
DB 181 MHVIVEKQLYNNHMGSDTTVAQKVFQGLIGNAIFVSNITIIISLSLELWIDENKIATTG 240
QY 241 EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGMCDANTAGGVVLHPRT 300
DB 241 EANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGATFQGMCDANTAGGVVLHPRT 300
QY 301 ISLESIAVILAOQLLSLGMITYDDINKCQCSGAVCIMNPEAIHPSGVKIFSNCSFEDFAH 360
DB 301 ISLESIAVILAOQLLSLGMITYDDINKCQCSGAVCIMNPEAIHPSGVKIFSNCSFEDFAH 360
QY 361 FISKQKSOQLHNPRLDPPFPKQAVCGNAKLEAGEECDCGTEQDCALIGTCCDIATCRF 420
DB 361 FISKQKSOQLHNPRLDPPFPKQAVCGNAKLEAGEECDCGTEQDCALIGTCCDIATCRF 420
QY 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQ 480
DB 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQ 480
QY 481 WICIDGCMGDKOCTDTFGKEVEFGPSECVSHLNSKTDVSGNGCISDSGYTQCEADNLQ 540
```

Db 481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLICKYVGKFLQIQIPRATIIYANISGHLICIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Db 541 CGKLICKYVGKFLQIQIPRATIIYANISGHLICIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Qy 601 RNQRCVSSSYLGVDCTTDCNDRGVGNKKHCHCSASYLPPDCSVQSDLPFGGSIDSGNF 660
Db 601 RNQRCVSSSYLGVDCTTDCNDRGVGNKKHCHCSASYLPPDCSVQSDLPFGGSIDSGNF 660
Qy 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIIFCVLIAMVKNFQKKWRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIIFCVLIAMVKNFQKKWRTEDY 720
Qy 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734
RESULT 3
ID ADB75186
XX ADB75186 standard; protein; 734 AA.
AC ADB75186;
XX ADB75186;
DT 04-DEC-2003 (first entry)
XX Prostate cancer marker protein.
XX Prostate; cancer; cytostatic; gene therapy; marker.
XX Homo sapiens.
OS
XX WO2003009814-A2.
XX
PD 06-FEB-2003.
XX
XX 25-JUL-2002; 2002WO-US023913.
XX
XX 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
XX WPI; 2003-248033/24.
XX
XX New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
XX
XX Disclosure; SEQ ID NO 10; 99pp; English.
XX
XX The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 734 AA;
Query Match 100.0%; Score 734; DB 7; Length 734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MWVLFLLSGLGGRMDSNFDLSLPVQITVPKIRSIIEGIESQASYSKIVIEGKYTVNLM 60
Db 1 MWVLFLLSGLGGRMDSNFDLSLPVQITVPKIRSIIEGIESQASYSKIVIEGKYTVNLM 60
Qy 61 QKQFLPNFRVYSVSGTGMKPLDDQDFQNFCHQYEGYGPXVMYSTCTGLRGVLQFE 120
Db 61 QKQFLPNFRVYSVSGTGMKPLDDQDFQNFCHQYEGYGPXVMYSTCTGLRGVLQFE 120
Qy 121 NVSYGIEPLESSVGFHVIYQVKHKADVSLYNEKDIESRDLSPKLSAEPQDFAKYIE 180
Db 121 NVSYGIEPLESSVGFHVIYQVKHKADVSLYNEKDIESRDLSPKLSAEPQDFAKYIE 180
Qy 181 MHVIVEKQLYNHMGSDTTVAQKVFQILGLTNAIFVSFNITIIILSSLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQKVFQILGLTNAIFVSFNITIIILSSLELWIDENKIATTG 240
Qy 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFQGMKCDANVAGGVVLPRT 300
Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFQGMKCDANVAGGVVLPRT 300
Qy 301 ISLES LAVILAQLLSLSMGITYDDINKCQSGAVCINMPEAIHFSGYKIFSNCSFEDFAH 360
Db 301 ISLES LAVILAQLLSLSMGITYDDINKCQSGAVCINMPEAIHFSGYKIFSNCSFEDFAH 360
Qy 361 FISKQSQCLHNPRLDPFPKQAVCNKLEAGEBCDCTQDCCALIGETCCDIATCRF 420
Db 361 FISKQSQCLHNPRLDPFPKQAVCNKLEAGEBCDCTQDCCALIGETCCDIATCRF 420
Qy 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQ 480
Db 421 KAGSNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQ 480
Qy 481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLICKYVGKFLQIQIPRATIIYANISGHLICIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Db 541 CGKLICKYVGKFLQIQIPRATIIYANISGHLICIAVEFASDHADSQKMWIKDGTSCGSKNVC 600
Qy 601 RNQRCVSSSYLGVDCTTDCNDRGVGNKKHCHCSASYLPPDCSVQSDLPFGGSIDSGNF 660
Db 601 RNQRCVSSSYLGVDCTTDCNDRGVGNKKHCHCSASYLPPDCSVQSDLPFGGSIDSGNF 660
Qy 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIIFCVLIAMVKNFQKKWRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSKPMRWPFLLFIPFFIIFCVLIAMVKNFQKKWRTEDY 720
Qy 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734
RESULT 4
AAR87034
ID AAR87034 standard; protein; 651 AA.
XX
AC AAR87034;
XX
DT 30-SEP-1996 (first entry)
XX
XX Human PH30 beta chain sperm protein.
XX
XX Human PH30 beta chain sperm protein; contraceptive;
KW FEE integrin binding domain.
XX
OS Homo sapiens.

XX WO9535118-A1.
XX 28-DEC-1995.
XX 06-JUN-1995; 95WO-US007295.
XX 20-JUN-1994; 94US-00264101.
XX (MERI) MERCK & CO INC.
XX Alves K, Gupta SK, Hollis GF;
XX WPI; 1996-058212/06.
XX N-PSDB; AAT36700.
XX Human and mouse sperm protein PH30 beta chain and related DNA - useful in
XX contraceptive vaccines.
XX Disclosure; Page 29-31; 85pp; English.
XX Human PH30 beta chain sperm protein, having an FEE integrin binding
XX domain, may be recombinantly produced by vector-mediated gene expression
XX in host cells, preferably mammalian cells e.g. Chinese hamster ovary
XX (CHO) cell culture. It may be used in a contraceptive composition
XX containing an effective adjuvant and an amount of sperm protein which is
XX effective for the stimulation of antibodies which bind to sperm protein
XX in vivo, thereby preventing or substantially reducing the rate of sperm-
XX egg fusion. The protein is also useful for identifying small molecules
XX that disrupt sperm-egg interaction and fertilization
XX Sequence 651 AA;
XX
XX Query Match 88.6%; Score 650; DB 2; Length 651;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 85 QDFQNFCHYQYIGYIPKSVVMVSTCTGLRGVLQFENVSVGIEPLESSVGFHEVIYQVKH 144
XX 2 QDFQNFCHYQYIGYIPKSVVMVSTCTGLRGVLQFENVSVGIEPLESSVGFHEVIYQVKH 61
XX
XX 145 KKADVSLYNEKDIESRDLSPKLSAEPQDPFQAKYIEMHVIIVEKOLYNHMGSDTTVAQKV 204
XX 62 KKADVSLYNEKDIESRDLSPKLSAEPQDPFQAKYIEMHVIIVEKOLYNHMGSDTTVAQKV 121
XX
XX 205 FOLIGLNLAI FVSFNITIISSLELWIDENKIATTGEANELLHTFLRWKTSYLVRPHDV 264
XX 122 FOLIGLNLAI FVSFNITIISSLELWIDENKIATTGEANELLHTFLRWKTSYLVRPHDV 181
XX
XX 265 AFLIVYREKSNVYGATFGKMCNDANYAGGVVLHPRITISLESILAVILAQLLSLMSGITYDD 324
XX 182 AFLIVYREKSNVYGATFGKMCNDANYAGGVVLHPRITISLESILAVILAQLLSLMSGITYDD 241
XX
XX 325 INKQCQSGAVCINMPEAIHFGSVKIFNCSPEDEPAHIFISKQSCQLNQRPLDPFFKQQA 384
XX 242 INKQCQSGAVCINMPEAIHFGSVKIFNCSPEDEPAHIFISKQSCQLNQRPLDPFFKQQA 301
XX
XX 385 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERMC 444
XX 302 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERMC 361
XX
XX 445 RPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQMVICIDGVCMSGDKQCTDTFGKEVE 504
XX 362 RPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQMVICIDGVCMSGDKQCTDTFGKEVE 421
XX
XX 505 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIKCVKGFLLQIPRATIYA 564
XX 422 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIKCVKGFLLQIPRATIYA 481
XX
XX 565 NISGHLICIAVEFASDHADSQKMWIKDGTSCGSKNVCRNQRVSSSYLGDCCTTDKCDNRG 624
XX 482 NISGHLICIAVEFASDHADSQKMWIKDGTSCGSKNVCRNQRVSSSYLGDCCTTDKCDNRG 541

Qy 625 VCNNKXCHCSASYLPPDCSVQSDLMFPGSGIDSGNPPVPAIPARLPERRRYENIYHSKPM 684
Db 542 VCNNKXCHCSASYLPPDCSVQSDLMFPGSGIDSGNPPVPAIPARLPERRRYENIYHSKPM 601
Qy 685 RWPFFLFIPIFFIIFCVLLIIMVKNQKWKRTEDYSSDQPESESEPKG 734
Db 602 RWPFFLFIPIFFIIFCVLLIIMVKNQKWKRTEDYSSDQPESESEPKG 651
RESULT 5
ADB75184
ID ADB75184 standard; protein; 735 AA.
XX
XX ADB75184;
XX
XX 04-DEC-2003 (first entry)
XX Prostate cancer marker protein.
XX Prostate; cancer; cytostatic; gene therapy; marker.
XX Homo sapiens.
XX PN W02003009814-A2.
XX PD 06-FEB-2003.
XX PF 25-JUL-2002; 2002WO-US023913.
XX PR 25-JUL-2001; 2001US-0307982P.
XX PR 22-AUG-2001; 2001US-0314356P.
XX PR 25-SEP-2001; 2001US-0325020P.
XX PR 12-DEC-2001; 2001US-0341746P.
XX PR 05-MAR-2002; 2002US-0362158P.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
XX Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX WPI; 2003-248033/24.
XX New nucleic acid molecule, useful for diagnosing or treating prostate
XX cancer.
XX Claim 4; SEQ ID NO 8; 99pp; English.
XX The invention relates to newly discovered cancer markers associated with
XX the cancerous state of prostate cells. Also disclosed is a method of
XX assessing whether a patient is afflicted with prostate cancer. The method
XX of the invention involves assessing whether a patient is afflicted with
XX prostate cancer by comparing the level of expression of a marker in a
XX patient sample and the normal level of expression of the marker in a
XX control non-prostate cancer sample, where a significant increase in the
XX level of expression of the marker in the patient sample and the normal
XX level indicates that the patient is afflicted with prostate cancer.
XX Nucleic acids of the invention are useful for diagnosing or treating
XX prostate cancer, and may be useful in gene therapy. Sequences given in
XX ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 735 AA;
XX
XX Query Match 86.0%; Score 631; DB 7; Length 735;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 3 VLFLLSLGLGRMDSNFDLPLVQITVPEKIRSIIRKIGIESQASYKIVIEGKPTVNLMOQ 62
XX 4 VLFLLSLGLGRMDSNFDLPLVQITVPEKIRSIIRKIGIESQASYKIVIEGKPTVNLMOQ 63

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QY 63 NPLPHNPRVYSYSGTGIMKPLDQDFQNFCHYQYIEGPKSVVMVSTCTGLRGVLQFENV 122
Db 64 NPLPHNPRVYSYSGTGIMKPLDQDFQNFCHYQYIEGPKSVVMVSTCTGLRGVLQFENV 123
QY 123 SYGIEPLESSVGFHEVYIYQVKKADVSLYNEKDIESRDLSPKLOSAEPQDDFAKYEIMH 182
Db 124 SYGIEPLESSVGFHEVYIYQVKKADVSLYNEKDIESRDLSPKLOSAEPQDDFAKYEIMH 183
QY 183 VIVEKQLYNHMGSDTTTVAQKVFQILGLTNAIPVSNITIIILSSLELWIDENKIATTEA 242
Db 184 VIVEKQLYNHMGSDTTTVAQKVFQILGLTNAIPVSNITIIILSSLELWIDENKIATTEA 243
QY 243 NEILLHFLRWKTSVILVLRPHDVAFLVYREKSNVVGATFGKMCMDANYAGGVILHPTIS 302
Db 244 NEILLHFLRWKTSVILVLRPHDVAFLVYREKSNVVGATFGKMCMDANYAGGVILHPTIS 303
QY 303 LESLAVILAQLLSLMSGITYDDINKKOCGAGVIMNPEALHFGSVKTFNSCSFEDPAHFI 362
Db 304 LESLAVILAQLLSLMSGITYDDINKKOCGAGVIMNPEALHFGSVKTFNSCSFEDPAHFI 363
QY 363 SKQKSQLHNPRLDPPFKQQAACVGNKLEAGEECDCGTEQDCALIGETCCDIATCRFKA 422
Db 364 SKQKSQLHNPRLDPPFKQQAACVGNKLEAGEECDCGTEQDCALIGETCCDIATCRFKA 423
QY 423 GSNCAEGPCENCLFMSKERMCRPSFECDLPRYCNCGSSASCENHYVQTHGPCGLNQWI 482
Db 424 GSNCAEGPCENCLFMSKERMCRPSFECDLPRYCNCGSSASCENHYVQTHGPCGLNQWI 483
QY 483 CIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG 542
Db 484 CIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG 543
QY 543 KLICKYVGFLLQIPRATIIYANISGHLCIAVEFASDHADSKQMWIKDGTSCGSKNVCYN 602
Db 544 KLICKYVGFLLQIPRATIIYANISGHLCIAVEFASDHADSKQMWIKDGTSCGSKNVCYN 603
QY 603 QRCVSSSYLGYDCTTKCDNDRGVNKKGHCHCSASYLPDDCSVQSDLWPGGSDSGNFP 662
Db 604 QRCVSSSYLGYDCTTKCDNDRGVNKKGHCHCSASYLPDDCSVQSDLWPGGSDSGNFP 663
QY 663 VAIPARUPERRYENIYHSPMRWPFLLPFPFTIFCVLAIAMVKNVFORKKWRTEDYSS 722
Db 664 VAIPARUPERRYENIYHSPMRWPFLLPFPFTIFCVLAIAMVKNVFORKKWRTEDYSS 723
QY 723 DEQPESESEPKG 734
Db 724 DEQPESESEPKG 735

RESULT 6
ADB75182
ID ADB75182 standard; protein; 753 AA.
XX AC ADB75182;
XX DT 04-DEC-2003 (first entry)
XX DE Prostate cancer marker protein.
XX KW Prostate; cancer; cytostatic; gene therapy; marker.
XX OS Homo sapiens.
XX PN WO2003009814-A2.
XX PD 06-FEB-2003.
XX PF 25-JUL-2002; 2002WO-US023913.
XX PR 25-JUL-2001; 2001US-0307982P.
XX PR 22-AUG-2001; 2001US-0314356P.
XX PR 25-SEP-2001; 2001US-0325020P.
XX PR 12-DEC-2001; 2001US-0341746P.
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PR 05-MAR-2002; 2002US-0362158P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B,
PI Hoerh S, Kamatkar S, Woneey AM, Glatt K, Zhao X, Anderson D;
XX WPI; 2003-248033/24.
XX New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
XX Claim 4; SEQ ID NO 6; 99pp; English.
PS The invention relates to newly discovered cancer markers associated with
XX the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 753 AA;
```

```
Query Match 83.0%; Score 609; DB 7; Length 753;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 QITVPEKIRSIIEGIESQASQYKIVIEGKPYTNLMQKNFLPHNFRVYSYSGTGIMKPLD 84
Db 44 QITVPEKIRSIIEGIESQASQYKIVIEGKPYTNLMQKNFLPHNFRVYSYSGTGIMKPLD 103
QY 85 QDFQNFCHYQYIEGPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFHEVYIYQVKH 144
Db 104 QDFQNFCHYQYIEGPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFHEVYIYQVKH 163
QY 145 KKADVSLYNEKDIESRDLSPKLOSAEPQDDFAKYEIMHIVEKQLYNHMGSDTTTVAQKV 204
Db 164 KKADVSLYNEKDIESRDLSPKLOSAEPQDDFAKYEIMHIVEKQLYNHMGSDTTTVAQKV 223
QY 205 FQILGLTNAIPVSNITIIILSSLELWIDENKIATTEGANELLTFLRWKTSYLVLRPHDV 264
Db 224 FQILGLTNAIPVSNITIIILSSLELWIDENKIATTEGANELLTFLRWKTSYLVLRPHDV 283
QY 265 AFLVYREKSNVYGATFGKMCMDANYAGGVILHPTISLESILAVILAQLLSLMSGITYDD 324
Db 284 AFLVYREKSNVYGATFGKMCMDANYAGGVILHPTISLESILAVILAQLLSLMSGITYDD 343
QY 325 INKQCQSGAVCINMPEALHFGSVKTFNSCSFEDFAHFISQKSQLHNPRLDPPFKQQA 384
Db 344 INKQCQSGAVCINMPEALHFGSVKTFNSCSFEDFAHFISQKSQLHNPRLDPPFKQQA 403
QY 385 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGNCNCAEGPCENCLFMSKERM 444
Db 404 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGNCNCAEGPCENCLFMSKERM 463
QY 445 RPSFECDLPEYCNCGSSASCENHYVQTHGPCGLNQMICIDGVCMSGDKQCTDTFGKEVE 504
Db 464 RPSFECDLPEYCNCGSSASCENHYVQTHGPCGLNQMICIDGVCMSGDKQCTDTFGKEVE 523
QY 505 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLI CKYVGFLLQIPRATIIYA 564
Db 524 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLI CKYVGFLLQIPRATIIYA 583
QY 565 NISGHLCIAVEFASDHADSKQMWIKDGTSCGSKNVCYNQRCVSSSYLGYDCTTKCDNDRG 624
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Db 584 NISGILCIAVEFASDHADSKWIKOGTSCGSKNVCNQCVCSSYLGXDCTDKNDRG 643
Qy 625 VCNKKKHCHCSASYLPDSCVQSDLPWPGGSDGNSFPFPAIPARLPERRIENIYHSPM 684
Db 644 VCNKKKHCHCSASYLPDSCVQSDLPWPGGSDGNSFPFPAIPARLPERRIENIYHSPM 703
Qy 685 RWPFFLPFPFIIFCVLIATMVKNFORKKWRTEYSSDQPESEPKG 734
Db 704 RWPFFLPFPFIIFCVLIATMVKNFORKKWRTEYSSDQPESEPKG 753

RESULT 7
AAE10823
ID AAE10823 standard; protein; 568 AA.
AC AAE10823;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human gene 2 encoded ADAM protein HOEK33, SEQ ID NO:7.
XX
KW Human; ADAM protein; a disintegrin and metalloprotease domain; cancer;
KW adamalysin; angiogenic disorder; chronic inflammatory disorder; ARDS;
KW rheumatoid arthritis; adult respiratory distress syndrome; asthma;
KW Crohn's disease; atherosclerosis; macular degeneration; psoriasis;
KW diabetic retinopathy; Alzheimer's disease; tissue remodeling;
KW haemorrhagic disorder; infertility; bone related disorder; stroke;
KW autoimmune disorder; haematopoietic disorder; infectious disease;
KW HIV-induced dementia; Human immunodeficiency virus; arrhythmia; epilepsy;
KW inflammatory bowel disease; cardiovascular disorder; renal disorder;
KW pulmonary disorder; central nervous system disorder;
KW respiratory disorder; obesity; cachexia; wasting disease; anorexia;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH Region 6..17
FT /note="Epitope"
FT 72..77
FT /note="Epitope"
FT 86..93
FT /note="Epitope"
FT 100..105
FT /note="Epitope"
FT 188..193
FT /note="Epitope"
FT 248..254
FT /note="Epitope"
FT 268..274
FT /note="Epitope"
FT 284..291
FT /note="Epitope"
FT 302..307
FT /note="Epitope"
FT 340..358
FT /note="Epitope"
FT 377..388
FT /note="Epitope"
FT 405..410
FT /note="Epitope"
FT 418..423
FT /note="Epitope"
FT 456..472
FT /note="Epitope"
FT 495..501
FT /note="Epitope"
FT 533..548
FT /note="Epitope"
FT 552..568
FT /note="Epitope"

PN WO200166557-A1.
XX 13-SEP-2001.
XX 22-FEB-2001; 2001WO-US005497.
XX 03-MAR-2000; 2000US-0187937P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Shi Y, Ruben SM;
PI WPI; 2001-596823/67.
XX N-PSDB; AAD18168.
DR Novel proteins comprising contain a disintegrin and metalloprotease
XX domain, referred as ADAM and ADAM polynucleotides for diagnosing,
PT preventing and treating cancer, inflammatory, reproductive,
PT cardiovascular disorders.
XX
PS Claim 11; Page 274-276; 280pp; English.
XX
CC AAD18167-AAD18170 represent cDNAs corresponding to human ADAM protein
CC (proteins which contain a disintegrin and metalloprotease domain, also
CC called adamalysins) genes, and AAE10822-AAE10825 represent the proteins
CC they encode. ADAM proteins and their corresponding genes are useful for
CC preventing, treating or ameliorating a medical condition in a mammal.
CC Sequences of the invention and their antibodies are useful for diagnosis,
CC and treatment of diseases related to angiogenic disorders such as cancer,
CC and cancer metastasis, chronic inflammatory disorders such as rheumatoid
CC arthritis, hepatitis, nephritis, Crohn's disease, asthma, adult
CC respiratory distress syndrome (ARDS), atherosclerosis, macular
CC degeneration, diabetic retinopathy, Alzheimer's disease, tissue
CC remodeling, psoriasis, haemorrhagic disorders, infertility, disorders
CC involving the skeletal system, reproductive system, bone related
CC disorders, autoimmune disorders, haematopoietic disorders, IGF-mediated
CC allergic reactions, organ transplant rejections, graft-versus-host
CC disease, infectious diseases, HIV-induced dementia, arrhythmias, high
CC blood pressure, muscular contractile dysfunction, pace-maker dysfunction,
CC disorder of proper neurotransmitter release, epilepsy, stroke, neural,
CC gastrointestinal (e.g. inflammatory bowel disease), cardiovascular (e.g.
CC myocarditis), renal, pulmonary, proliferative, respiratory (e.g. allergy)
CC disorders and/or cancerous diseases or conditions such as gastric, lung,
CC ovarian, bladder, liver and breast), central nervous system disorders
CC (e.g. prion disease) and/or hormone secretion disorders. ADAM genes,
CC proteins, agonists or antagonist prevents skin aging due to sunburn,
CC modulate the differentiation or proliferation of embryonic stem cells,
CC modulate mammalian characteristics such as body height, weight, hair
CC colour, skin, modulate mammalian metabolism, biornhms and are useful
CC for treating obesity, cachexia, wasting disease, anorexia and bulimia.
CC They are also useful as food additive or preservative to increase or
CC decrease storage capabilities, fat content, lipid, protein or other
CC nutritional components. Polynucleotides of the invention are useful in
CC gene therapy. The present sequence represents a human ADAM protein of the
CC invention
XX
SQ Sequence 568 AA;

Query Match 2.0%; Score 15; DB 4; Length 568;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 117 LQFENVSYGIEPLES 131
Db 47 LQFENVSYGIEPLES 61
RESULT 8
ABJ26664
ID ABJ26664 standard; protein; 668 AA.
XX
AC ABJ26664;
XX

DT XX 01-MAY-2003 (first entry)
DE XX Human protein modification + maintenance molecule protein SEQ ID No 18.
XX XX Cystostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
XX KW cerebroprotective; antiparkinsonian; nootropic; antiinflammatory;
XX KW antitumor; hepatotropic; gynecological; antibacterial; virucide;
XX KW protozoacide; antiparasitic; cell proliferative disease; PMOD;
XX KW protein modification and maintenance molecule; immunogenic fragment;
XX KW cancer; autoimmune; inflammatory disease; neurological disorder;
XX KW gastrointestinal; developmental; vesicle trafficking disorder; infection;
XX KW protein-protein interaction; drug-target interaction;
XX KW gene expression profile; human.
XX XX Homo sapiens.
OS XX WO2003000844-A2.
XX XX 03-JAN-2003.
XX XX 18-JUN-2002; 2002WO-US019360.
XX XX 22-JUN-2001; 2001US-0300508P.
XX PR 06-JUL-2001; 2001US-0303445P.
XX PR 13-JUL-2001; 2001US-0305405P.
XX PR 09-AUG-2001; 2001US-0311442P.
XX PR 24-AUG-2001; 2001US-0314821P.
XX PR 29-AUG-2001; 2001US-0315992P.
XX PR 03-MAY-2002; 2002US-0378205P.
XX XX (INCY-) INCYTE GENOMICS INC.
XX XX Gandhi AR, Kable AB, Swarnakar A, Hafalia AJA, Tran B, Duggan BM;
XX PI Warren BA, Ison CH, Honeckell CD, Nguyen DB, Lu DAM, Lee EA, Yue H;
XX PI Forsythe IJ, Barroso I, Rankumar J, Griffin JA, Li JX, Yang J;
XX PI Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG;
XX PI Wallia NK, Mason PM, Gururajan R, Lee S, Becha SD, Tran UK;
XX PI Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebrafadian Y;
XX XX WPI; 2003-184039/18.
XX DR N-PSDB; ABT23217.
XX XX New isolated human PMOD polypeptide and polynucleotide, useful for
XX PT diagnosing, treating and preventing diseases or conditions associated
XX PT with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis and
XX PT infections.
XX XX Claim 73; Page 193-194; 225pp; English.
XX XX The invention relates to an isolated polypeptide comprising: any of 28
XX CC sequences of 48-1256 amino acids; a natural amino acid sequence at least
XX CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence
XX CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino
XX CC acids, or 9% identical to a sequence of 242 amino acids, all given in
XX CC the specification; or a biologically active or immunogenic fragment of
XX CC the isolated polypeptide. The polypeptides and polynucleotides are useful
XX CC in diagnosing, treating and preventing diseases or conditions associated
XX CC with the decreased expression of protein modification and maintenance
XX CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer,
XX CC atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS,
XX CC allergies), neurological disorders (e.g. stroke, Parkinson's disease,
XX CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g.
XX CC endometriosis), developmental, vesicle trafficking disorders, and
XX CC infections (e.g. bacterial, viral, parasitic, protozoal). These are also
XX CC useful in assessing the effects of exogenous compounds on the expression
XX CC of nucleic acid and amino acid sequences of PMOD. The PMOD or its
XX CC fragments are useful in screening compounds for effectiveness as agonist
XX CC or antagonist of the polypeptides, or in altering the expression of the
XX CC target polynucleotide and compounds that specifically bind to or modulate
XX CC the activity of the polypeptide. The microarray is useful in monitoring
XX CC or measuring protein-protein interactions, drug-target interactions, and
XX CC gene expression profiles. This sequence represents a human PMOD protein
XX CC of the invention

XX SQ Sequence 668 AA;
XX XX Query Match 2.0%; Score 15; DB 6; Length 668;
XX XX Best Local Similarity 100.0%; Pred. No. 1.7e-05; Indels 0;
XX XX Matches 15; Conservative 0; Mismatches 0; Gaps 0;
XX XX
XX Qy 117 LQFENVSYGIEPLES 131
XX Db 121 LQFENVSYGIEPLES 135
XX XX
XX RESULT 9
XX ID AAU97037 standard; protein; 759 AA.
XX XX AC AAU97037;
XX XX DT 13-AUG-2002 (first entry)
XX XX DE Human LP protein LP102.
XX KW Human; LP102; inflammatory disorder; diabetes; bone disease;
XX KW cardiovascular disease; male reproductive system disease; osteoporosis;
XX KW Paget's disease; myeloma; Alzheimer's disease; contraceptive;
XX KW liver cancer; growth factor-mediated disease; anaphylaxis; coagulation;
XX KW sepsis; skeletal muscle dystrophy; asthma; breast cancer.
XX OS Homo sapiens.
XX PN WO200232939-A2.
XX XX 25-APR-2002.
XX XX 10-OCT-2001; 2001WO-US027759.
XX XX 19-OCT-2000; 2000US-0241813P.
XX XX (ELIL) LILLY & CO ELI.
XX XX Lu D, Song HY, Su EW, Wang H;
XX XX WPI; 2002-454591/48.
XX DR N-PSDB; ABK51494.
XX XX New secreted human LP polypeptides or polynucleotides, useful for
XX PT treating mammals suffering from conditions associated with aberrant
XX PT levels of an LP polypeptide, e.g. cancers, osteoporosis, Paget's disease
XX PT or Alzheimer's disease.
XX XX Claim 8; Page 131-134; 148pp; English.
XX CC The invention relates to isolated human polypeptides designated LP102,
XX CC LP187, LP190 and LP241, and the polynucleotides encoding them. The LP
XX CC polypeptide or the LP polypeptide agonist is useful for treating a mammal
XX CC suffering from a disease, condition or disorder associated with aberrant
XX CC levels of an LP polypeptide. The LP polypeptides or polynucleotides, or
XX CC the antibodies are useful for treating, preventing or diagnosing cancers,
XX CC inflammatory disorders, bone diseases or cardiovascular diseases. In
XX CC particular, the LP102 polypeptides, polynucleotides or antibodies are
XX CC useful for diagnosing, preventing or treating male reproductive system
XX CC diseases, osteoporosis, Paget's disease, metastatic or myeloma associated
XX CC bone diseases or Alzheimer's disease. These are also useful as
XX CC contraceptive agents. The LP187 polypeptides, polynucleotides or
XX CC antibodies are particularly useful for diagnosing, preventing or treating
XX CC liver cancer, as well as other growth factor-mediated diseases and
XX CC conditions. The LP190 polypeptides, polynucleotides or antibodies are
XX CC useful for diagnosing, preventing or treating asthma, anaphylaxis, and
XX CC diseases related to coagulation or sepsis. LP241 polypeptides,
XX CC polynucleotides or antibodies are useful especially for diagnosing,
XX CC preventing or treating skeletal muscle dystrophy, breast cancer or
XX CC diabetes. The LP polynucleotides are also useful for constructing DNA
XX CC vectors that may be employed in medicine, or for preparing the proteins.

CC The present sequence represents the amino acid sequence of LP102

XX Sequence 759 AA;

Query Match 2.0%; Score 15; DB 5; Length 759;

Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131

Db 121 LQFENVSYGIEPLES 135

RESULT 10

AAU83636

ID AAU83636 standard; protein; 787 AA.

AC AAU83636;

XX 08-MAY-2002 (first entry)

DE Human PRO protein, Seq ID No 90.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

KW breast cancer; prostate tumour; rectal tumour; liver tumour;

KM pericyte cell proliferation; chondrocyte cell proliferation;

KW tumour necrosis factor-alpha.

XX Homo sapiens.

XX WO200208288-A2.

XX 31-JAN-2002.

PF 29-JUN-2001; 2001WO-US021066.

XX 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220585P.

PR 25-JUL-2000; 2000US-0220605P.

PR 25-JUL-2000; 2000US-0220607P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220638P.

PR 25-JUL-2000; 2000US-0220664P.

PR 25-JUL-2000; 2000US-0220666P.

PR 26-JUL-2000; 2000US-0220893P.

PR 28-JUL-2000; 2000WO-US020710.

PR 01-AUG-2000; 2000US-0222425P.

PR 22-AUG-2000; 2000US-0227133P.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 10-NOV-2000; 2000WO-US030873.

PR 28-NOV-2000; 2000US-0253646P.

PR 01-DEC-2000; 2000WO-US032878.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006566.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 25-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001WO-US017092.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2002-172001/22.

DR N-PSDB; ABK33580.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,

PT useful for treating a PRO related disorder and for diagnosing tumors such

PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor

PT or liver tumor.

XX Claim 11; Fig 90; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention

XX SQ Sequence 787 AA;

Query Match 2.0%; Score 15; DB 5; Length 787;

Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131

Db 121 LQFENVSYGIEPLES 135

RESULT 11

ABU80783

ID ABU80783 standard; protein; 787 AA.

XX AC ABU80783;

XX 23-JUN-2003 (first entry)

XX Human PRO polypeptide #45.

XX Human; PRO polypeptide; secreted and transmembrane protein;

KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.

XX Homo sapiens.

XX US2003036635-A1.

XX 20-FEB-2003.

XX 28-AUG-2002; 2002US-00230163.

XX 25-JUL-2000; 2000US-0220638P.

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-342045/32.

DR N-PSDB; ACA66885.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,

PT useful for the manufacture of a medicament for diagnosing or treating

PT tumor.

XX Claim 11; Fig 90; 314pp; English.

XX The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a medicament
 CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
 CC useful in diagnostic assays for PRO, by detecting its expression in
 CC specific cells, tissues or serum, and for affinity purification of PRO
 CC from recombinant cell culture or natural sources. AB080739-AB080860
 CC represent the human PRO polypeptides of the invention. Note: The sequence
 CC data for this patent was obtained in electronic format directly from the
 CC USPTO web site at seqdata.uspto.gov/psipdIDEntry.html
 XX
 SQ Sequence 787 AA;

Query Match 2.0%; Score 15; DB 6; Length 787;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131
 DB 121 LQFENVSYGIEPLES 135
 |||||

RESULT 12
 AB033749
 ID AB033749 standard; protein; 787 AA.

XX AC AB033749;

XX DT 17-SEP-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO21340.

XX Human; secreted and transmembrane protein; PRO; cytostatic;
 KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
 KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
 KW pharmaceutical; diagnostic; biosensor; bioresactor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; bone disorder; cartilage disorder; sports injury;
 KW arthritis; wound.

XX OS Homo sapiens.

XX PN US2003045687-A1.

XX PD 06-MAR-2003.

XX PF 12-AUG-2002; 2002US-00218631.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX XX WPI; 2003-512315/48.

XX DR N-PSDB; ACD68637.

XX New genes, and its encoded secreted and transmembrane polypeptides,
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
 PT pericyte proliferation, especially for treating lung tumors, arthritis or
 PT wounds in a mammal.

XX PS Claim 11; Fig 90; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 CC fully defined in the specification; or (b) any of 122 nucleotide
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 CC specification; or the full length coding sequence of any of these 122

CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting tumours (e.g. lung tumour, colon
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells, for stimulating proliferation of pericyte cells, or for modulating
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
 CC polypeptide is also useful for treating tumours or various bone and/or
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 SQ Sequence 787 AA;

Query Match 2.0%; Score 15; DB 6; Length 787;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131
 DB 121 LQFENVSYGIEPLES 135
 |||||

RESULT 13
 AB082092

ID AB082092 standard; protein; 787 AA.

XX AC AB082092;

XX DT 25-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO21340.

XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN US2003088063-A1.

XX PD 08-MAY-2003.

XX PF 12-AUG-2002; 2002US-00219003.

XX PR 25-JUL-2000; 2000US-0220664P.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-393229/37.

XX DR N-PSDB; ACA68541.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 11; Fig 90; 314pp; English.
 XX
 CC The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This is the amino acid
 CC sequence of a novel human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 787 AA;
 Query Match 2.0%; Score 15; DB 6; Length 787;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 LQFENVSYGIEPLES 131
 Db 121 LQFENVSYGIEPLES 135
 |||||
 RESULT 14
 ABR48487
 ID ABR48487 standard; protein; 787 AA.
 XX
 AC ABR48487;
 DT 13-JUN-2003 (first entry)
 XX
 DX Human LAP cell surface protein.
 DE Human; GENSET; therapeutic; therapy.
 XX
 KW Homo sapiens.
 OS
 XX
 XX W0200294864-A2.
 PN
 XX 28-NOV-2002.
 PD
 XX 06-AUG-2001; 2001WO-IB001715.
 PF
 XX 25-MAY-2001; 2001US-0293574P.
 PR 15-JUN-2001; 2001US-0298698P.
 PR 29-JUN-2001; 2001US-0302277P.
 PR 13-JUL-2001; 2001US-0305456P.
 XX
 XX (GEST) GENSET.
 PA
 XX
 XX Bejanin S, Tanaka H;
 PI
 XX WPI; 2003-129412/12.
 DR
 DR N-PSDB; ACC51094.
 XX
 XX New GENSET polynucleotides and polypeptides, useful for preparing a
 PT composition for treating GENSET-related disorders and as reagents in
 PT assays to quantitatively determined levels of GENSET expression in
 PT biological samples.
 XX
 XX Claim 2; Page 462-463; 505pp; English.
 PS
 XX The present invention relates to novel human GENSET coding sequences
 CC (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
 CC sequences are useful for preparing a composition for treating GENSET-
 CC related disorders. They can also be used as markers for tissues in which
 CC the corresponding protein is preferentially expressed, as molecular
 CC weight markers on Southern gels, as chromosome markers or tags to

CC identify chromosomes, and as reagents in assays to quantitatively
 CC determined levels of GENSET expression in biological samples
 XX
 SQ Sequence 787 AA;
 Query Match 2.0%; Score 15; DB 6; Length 787;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 LQFENVSYGIEPLES 131
 Db 121 LQFENVSYGIEPLES 135
 |||||
 RESULT 15
 ABR72272
 ID ABR72272 standard; protein; 787 AA.
 XX
 AC ABR72272;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DX Human PRO21340 protein.
 DE
 XX PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
 KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 XX US2003050448-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 28-AUG-2002; 2002US-00230414.
 PF
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX N-PSDB; ABT44270.
 DR
 DR WPI; 2003-521818/49.
 DR
 XX New nucleic acid encoding for a PRO protein, useful for the manufacture
 PT of a medicament for diagnosing or treating tumors or for measuring or
 PT detecting expression of an associated gene.
 XX
 XX Claim 11; Fig 90; 315pp; English.
 PS
 XX The invention relates to a novel isolated nucleic acid encoding a fully
 CC defined PRO polypeptide. The molecules of the invention may be useful for
 CC stimulating proliferation or gene expression in pericyte cells or the
 CC release of TNF-alpha from human blood. Other possible uses include the
 CC stimulation or inhibition of chondrocyte proliferation or
 CC differentiation, the stimulation of human dermal fibroblast cell
 CC proliferation and the detection of the presence of a tumour within a
 CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
 CC of a medicament for diagnosing or treating a tumour within a mammal or
 CC for measuring or detecting the expression of an associated gene, as well
 CC as during gene therapy. The current sequence is that of the human PRO
 CC protein of the invention.
 XX
 SQ Sequence 787 AA;
 Query Match 2.0%; Score 15; DB 6; Length 787;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 LQFENVSYGIEPLES 131

Db |||||||
 121 LQFENVSYGIEPLES 135

Search completed: January 10, 2005, 22:34:38
Job time : 162 secs

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	Query Match	100.0%	Score 734;	DB 14;	Length 734;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 734;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	MMWFLLSGGGLGRMDSNFDPSLPVQIITVPEKIRSIIEGIESQASYKIVIEGKPYTNLM			
Db	1	MMWFLLSGGGLGRMDSNFDPSLPVQIITVPEKIRSIIEGIESQASYKIVIEGKPYTNLM			
Qy	61	QKNFLPHNFVYSYSGTGIMKPLDQDQFQNFCHQYIEGYPKSVVMVSTCTGLRGVLQFE			

Db 61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE 120
QY 121 NVSYGIEPLESSYGFHVIYQVXHKADVSLYNEKDIIESRDLGFKLOSAPQODFAKYIE 180
Db 121 NVSYGIEPLESSYGFHVIYQVXHKADVSLYNEKDIIESRDLGFKLOSAPQODFAKYIE 180
QY 181 MHVIVEKQLYNHMGSDTTVAQKVFQGLIGLNAIFVSNFTIILSSLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQKVFQGLIGLNAIFVSNFTIILSSLELWIDENKIATTG 240
QY 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYVATFQGMKCDANVAGGVWLHPRT 300
Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYVATFQGMKCDANVAGGVWLHPRT 300
QY 301 ISLES LAVILAQLLSLSMGITDIDINKCQSGAVCINMPEAIHFGSVKIFSNCSFEDFAH 360
Db 301 ISLES LAVILAQLLSLSMGITDIDINKCQSGAVCINMPEAIHFGSVKIFSNCSFEDFAH 360
QY 361 FISKQSQCLHNPRLDPPFKQAQVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
Db 361 FISKQSQCLHNPRLDPPFKQAQVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
QY 421 KAGSNCAEGPCCCNCLFMSKERMCRPSFECDLPEYCNCGSSASC PENHYVOTGHPCLNQ 480
Db 421 KAGSNCAEGPCCCNCLFMSKERMCRPSFECDLPEYCNCGSSASC PENHYVOTGHPCLNQ 480
QY 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
QY 541 CGKLI CKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKWKIKDGTSCGSKNVC 600
Db 541 CGKLI CKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKWKIKDGTSCGSKNVC 600
QY 601 RNORCVSSSYLVGYDCTTDKNDRGVCNNKHKCHCSASYLPDSCVSQDLWPGGSDSGNF 660
Db 601 RNORCVSSSYLVGYDCTTDKNDRGVCNNKHKCHCSASYLPDSCVSQDLWPGGSDSGNF 660
QY 661 PPVAIPARLPERRYENIYHSPKMRWPFLLFIPFFIIFCVLIAIMVKVNFQKWKRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSPKMRWPFLLFIPFFIIFCVLIAIMVKVNFQKWKRTEDY 720
QY 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734

RESULT 2

US-10-205-823-10
; Sequence 10, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wensey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-205-823-10
Query Match 100.0%; Score 734; DB 14; Length 734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVLFLSLGLGLRMDNSFDSLPVQITVPEKIRSIIEGIESQASYKIVIEGKPYTNLM 60
Db 1 MVLFLSLGLGLRMDNSFDSLPVQITVPEKIRSIIEGIESQASYKIVIEGKPYTNLM 60
QY 61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE 120
Db 61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFE 120
QY 121 NVSYGIEPLESSYGFHVIYQVXHKADVSLYNEKDIIESRDLGFKLOSAPQODFAKYIE 180
Db 121 NVSYGIEPLESSYGFHVIYQVXHKADVSLYNEKDIIESRDLGFKLOSAPQODFAKYIE 180
QY 181 MHVIVEKQLYNHMGSDTTVAQKVFQGLIGLNAIFVSNFTIILSSLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQKVFQGLIGLNAIFVSNFTIILSSLELWIDENKIATTG 240
QY 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYVATFQGMKCDANVAGGVWLHPRT 300
Db 241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNVYVATFQGMKCDANVAGGVWLHPRT 300
QY 301 ISLES LAVILAQLLSLSMGITDIDINKCQSGAVCINMPEAIHFGSVKIFSNCSFEDFAH 360
Db 301 ISLES LAVILAQLLSLSMGITDIDINKCQSGAVCINMPEAIHFGSVKIFSNCSFEDFAH 360
QY 361 FISKQSQCLHNPRLDPPFKQAQVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
Db 361 FISKQSQCLHNPRLDPPFKQAQVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRF 420
QY 421 KAGSNCAEGPCCCNCLFMSKERMCRPSFECDLPEYCNCGSSASC PENHYVOTGHPCLNQ 480
Db 421 KAGSNCAEGPCCCNCLFMSKERMCRPSFECDLPEYCNCGSSASC PENHYVOTGHPCLNQ 480
QY 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
QY 541 CGKLI CKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKWKIKDGTSCGSKNVC 600
Db 541 CGKLI CKYVGKFLLOIPRATIIYANISGHLCIAVEFASDHADSQKWKIKDGTSCGSKNVC 600
QY 601 RNORCVSSSYLVGYDCTTDKNDRGVCNNKHKCHCSASYLPDSCVSQDLWPGGSDSGNF 660
Db 601 RNORCVSSSYLVGYDCTTDKNDRGVCNNKHKCHCSASYLPDSCVSQDLWPGGSDSGNF 660
QY 661 PPVAIPARLPERRYENIYHSPKMRWPFLLFIPFFIIFCVLIAIMVKVNFQKWKRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSPKMRWPFLLFIPFFIIFCVLIAIMVKVNFQKWKRTEDY 720
QY 721 SSDEQPESESEPKG 734
Db 721 SSDEQPESESEPKG 734

RESULT 3

US-10-473-603-19


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Db 244 NELLHFLRWKTSYLVLRPHDVAFLVYREKSNVGTATFGKMCNDANYAGGVVLRPTIS 303
QY 303 LESLAVILAQLLSLSMGITYDDINKQCAGVACIMNPEAIHFGVKIFNCSFEDFAHFI 362
Db 304 LESLAVILAQLLSLSMGITYDDINKQCAGVACIMNPEAIHFGVKIFNCSFEDFAHFI 363
QY 363 SKOKSCLHNOPRLDFFKQOAVCGNAKLEAGECDGTEODCALIGETCCDIATCRFXA 422
Db 364 SKOKSCLHNOPRLDFFKQOAVCGNAKLEAGECDGTEODCALIGETCCDIATCRFXA 423
QY 423 GSNCAAGPCCENCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPCGLNQWI 482
Db 424 GSNCAAGPCCENCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPCGLNQWI 483
QY 483 CIDGVCMSGDGKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG 542
Db 484 CIDGVCMSGDGKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG 543
QY 543 KLIKCVGKFLQIPRATIIYANISGHLCTAVFASDHADSQKWKIKDGTSCGSNKVCRN 602
Db 544 KLIKCVGKFLQIPRATIIYANISGHLCTAVFASDHADSQKWKIKDGTSCGSNKVCRN 603
QY 603 QRCVSSSYLYGCDTCTDKCNDRGVGNKKKHCHCSASYLPDPCSVQSDLWPGGSDSGNFP 662
Db 604 QRCVSSSYLYGCDTCTDKCNDRGVGNKKKHCHCSASYLPDPCSVQSDLWPGGSDSGNFP 663
QY 663 VAIPARLPERRYENIYHSPMRWPFPLFPFIIFCVLIAMVKNVFORKKWRTEDYSS 722
Db 664 VAIPARLPERRYENIYHSPMRWPFPLFPFIIFCVLIAMVKNVFORKKWRTEDYSS 723
QY 723 DEQPESESEPKG 734
Db 724 DEQPESESEPKG 735
```

RESULT 5

```
US-10-205-823-6
; Sequence 6, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Maniula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 753
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-205-823-6
Query Match 83.0%; Score 609; DB 14; Length 753;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 QITVPEKRSIIKEGIESQASYKIVIEGKPYTVNLQKQNFPHNFRVYSYSGTGMKPLD 84
Db 44 QITVPEKRSIIKEGIESQASYKIVIEGKPYTVNLQKQNFPHNFRVYSYSGTGMKPLD 103
QY 85 QDFQNFCHYQGYIEGYEYKPSVVMVSTCTGLRGVLQENVSYGIEPLESSVGFPHYIYQV 144
Db 104 QDFQNFCHYQGYIEGYEYKPSVVMVSTCTGLRGVLQENVSYGIEPLESSVGFPHYIYQV 163
QY 145 KKADVSLYNEKDIERSDLFSKLOSAPQODFAKYIEMHVIVVEKOLYNHMGSDTTVVAAKV 204
Db 164 KKADVSLYNEKDIERSDLFSKLOSAPQODFAKYIEMHVIVVEKOLYNHMGSDTTVVAAKV 223
QY 205 FOLIGLTNAIFVSNITITILSSLELWIDENKIATTEANELLHTFLRWKTSYLVLRPHDV 264
Db 224 FOLIGLTNAIFVSNITITILSSLELWIDENKIATTEANELLHTFLRWKTSYLVLRPHDV 283
QY 265 AFLVYREKSNVGTATFGKMCNDANYAGGVVLRPTISLESILAVILAQLLSLSMGITYDD 324
Db 284 AFLVYREKSNVGTATFGKMCNDANYAGGVVLRPTISLESILAVILAQLLSLSMGITYDD 343
QY 325 INKCCSGGAVCIMNPEAIHFGVKIFSNCSFEDFAHFIKQSKQCLHNOPRLDPPFKQQA 384
Db 344 INKCCSGGAVCIMNPEAIHFGVKIFSNCSFEDFAHFIKQSKQCLHNOPRLDPPFKQQA 403
QY 385 VCGNAKLEAGECDGTEODCALIGETCCDIATCRFKAGSNCAEGCCENCLFMSKERM 444
Db 404 VCGNAKLEAGECDGTEODCALIGETCCDIATCRFKAGSNCAEGCCENCLFMSKERM 463
QY 445 RPSFECDLPEYCNCGSSASCENHYVOTGHPCGLNQWICIDGVCMSGDGKQCTDTFGKEVE 504
Db 464 RPSFECDLPEYCNCGSSASCENHYVOTGHPCGLNQWICIDGVCMSGDGKQCTDTFGKEVE 523
QY 505 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIKCYVGKFLQIPRATIIYA 564
Db 524 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIKCYVGKFLQIPRATIIYA 583
QY 565 NISGHLCTIAVEFASDHADSQKWKIKDGTSCGSNKVCRNORCVSSSYLYGDCITDKCNDRG 624
Db 584 NISGHLCTIAVEFASDHADSQKWKIKDGTSCGSNKVCRNORCVSSSYLYGDCITDKCNDRG 643
QY 625 VCNKKKHCHCSASYLPDPCSVQSDLWPGGSDSGNFPVAIPARLPERRYENIYHSPKM 684
Db 644 VCNKKKHCHCSASYLPDPCSVQSDLWPGGSDSGNFPVAIPARLPERRYENIYHSPKM 703
QY 685 RWPFFLPFPFIIFCVLIAMVKNVFORKKWRTEDYSSDEQPESESEPKG 734
Db 704 RWPFFLPFPFIIFCVLIAMVKNVFORKKWRTEDYSSDEQPESESEPKG 753
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RESULT 6

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US-09-945-676-7
; Sequence 7, Application US/09945676
; Patent No. US20020077465A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT051P1
; CURRENT APPLICATION NUMBER: US/09/945,676
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PCT/US01/05497
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/187,937
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
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; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-676-7

Query Match          2.0%; Score 15; DB 9; Length 568;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131
Db 47 LQFENVSYGIEPLES 61

RESULT 7
US-10-381-820A-2
; Sequence 2; Application US/10381820A
; Publication No. US20040142333A1
; GENERAL INFORMATION:
; APPLICANT: Dethun, Lu
; APPLICANT: Song, Ho Yeong
; APPLICANT: Su, Eric Wen
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel Secreted Proteins and Their Uses
; FILE REFERENCE: X-13974
; CURRENT APPLICATION NUMBER: US/10/381,820A
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-381-820A-2

Query Match          2.0%; Score 15; DB 16; Length 759;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131
Db 121 LQFENVSYGIEPLES 135

RESULT 8
US-09-992-600A-70
; Sequence 70; Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Jpatent
; SEQ ID NO 70
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match          2.0%; Score 15; DB 10; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131
Db 121 LQFENVSYGIEPLES 135

RESULT 9
US-09-924-340-70
; Sequence 70; Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Jpatent
; SEQ ID NO 70
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-340-70

Query Match          2.0%; Score 15; DB 10; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131
Db 121 LQFENVSYGIEPLES 135

RESULT 10
US-09-992-095B-70
; Sequence 70; Application US/09992095B
; Publication No. US20030157485A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US5.DIV
; CURRENT APPLICATION NUMBER: US/09/992,095B
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
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;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: JPatent
;; SEQ ID NO 70
;; LENGTH: 787
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..16
US-09-992-095B-70

Query Match 2.0%; Score 15; DB 10; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LQFENVSYGIEPLES 131
Db 121 LQFENVSYGIEPLES 135

RESULT 11
US-09-999-570-70
;; Sequence 70, Application US/09999570
;; Publication No. US20030170628A1
;; GENERAL INFORMATION:
;; APPLICANT: Benjamin, Stephane
;; APPLICANT: Tanaka, Hiroaki
;; TITLE OF INVENTION: HUMAN CNAS AND PROTEINS AND USES THEREOF
;; FILE REFERENCE: G-091US08DIV
;; CURRENT APPLICATION NUMBER: US/09/999,570
;; CURRENT FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: US 09/924,340
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: PCT/IB01/01715
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: US 60/305,456
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/302,277
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 60/298,698
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: JPatent
;; SEQ ID NO 70
;; LENGTH: 787
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..16
US-09-999-570-70

Query Match 2.0%; Score 15; DB 10; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LQFENVSYGIEPLES 131
Db 121 LQFENVSYGIEPLES 135

RESULT 12
US-10-227-884-90
;; Sequence 90, Application US/10227884
;; Publication No. US20030027988A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stephan, Jean-Philippe F.
;; APPLICANT: Watanabe, Colin L.
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3530PIC79
;; CURRENT APPLICATION NUMBER: US/10/227,884
;; CURRENT FILING DATE: 2002-08-26
;; PRIOR APPLICATION NUMBER: 10/119,480
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/062287
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063549
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/064103
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/069873
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086392
;; PRIOR FILING DATE: 1998-05-22
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;; PRIOR APPLICATION NUMBER: 60/089905
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090691
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/095302
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095318
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095916
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/096146
;; PRIOR FILING DATE: 1998-08-11
;; PRIOR APPLICATION NUMBER: 60/096791

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; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/099812
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
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; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10

;
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 2.0%; Score 15; DB 14; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LQFENVSYGIEPLES 131
| | | | | | | | | | | | | | | | | | | | | |
Db 121 LQFENVSYGIEPLES 135

RESULT 13
US-10-230-163-90
; Sequence 90, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C96
CURRENT APPLICATION NUMBER: US/10/230,163
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
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PRIOR APPLICATION NUMBER: 60/091982
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PRIOR APPLICATION NUMBER: 60/095318
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PRIOR APPLICATION NUMBER: 60/095916
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PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
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PRIOR APPLICATION NUMBER: 60/099816
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PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
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PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
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PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
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PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
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PRIOR FILING DATE: 1998-11-17
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PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
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PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
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; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
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; PRIOR APPLICATION NUMBER: 60/164418
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; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
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; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 2.0%; Score 15; DB 14; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 117 LQFENVSYGIEPLES 131
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Db 121 LQFENVSYGIEPLES 135

RESULT 14
US-10-230-338-90
; Sequence 90, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C92
; CURRENT FILING DATE: 2002-08-28

; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 90
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-90

Query Match 2.0%; Score 15; DB 14; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 117 LQFENVSYGIEPLES 131
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Db 121 LQFENVSYGIEPLES 135

RESULT 15
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; Sequence 90, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 22:29:24 ; Search time 40 Seconds
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1216.935 Million cell updates/sec

Title: US-10-054-683-19

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	734	100.0	734	5	PCT-US95-07295-8
3	650	88.6	651	1	US-08-264-101-2
4	650	88.6	651	2	US-08-765-243-2
5	650	88.6	651	5	PCT-US95-07295-2
6	15	2.0	787	4	US-10-000-489-70
7	12	1.6	48	5	PCT-US93-05640-34
8	12	1.6	50	5	PCT-US93-05640-16
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16	10	1.4	68	4	US-09-243-640-14
17	10	1.4	68	4	US-08-929-847-16
18	10	1.4	68	4	US-09-813-484-16
19	10	1.4	71	1	US-07-965-674-8
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25	9	1.2	71	4	US-09-460-295B-7
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33	9	1.2	73	4	US-09-460-295B-10	Sequence 10, Appli
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45	9	1.2	98	1	US-07-623-611-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-08-765-243-8

; Sequence 8, Application US/08765243

; Patent No. 5935578

; GENERAL INFORMATION:

; APPLICANT: ALVES, KENNETH

; APPLICANT: GUPTA, SUNIL K.

; APPLICANT: HOLLIS, GREGORY F.

; TITLE OF INVENTION: CONTRACEPTIVE VACCINE

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MARY A. APPOLLINA

; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

; CITY: RAYWAY

; STATE: NJ

; COUNTRY: USA

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/765,243

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: APPOLLINA, MARY A

; REGISTRATION NUMBER: 34,087

; REFERENCE/DOCKET NUMBER: 19244Y

; TELEPHONE: (908)594-3462

; TELEFAX: (908)594-4720

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 734 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-765-243-8

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Db	1	MWVFLSLGGLGRMDSNFDLPVQITVPKIRSIKEGIESQASYSKIVIEGKPYTNLM	60	
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Db 121 NVSYGIEPLESSVGFHEVIYQVGHKADVSLYNEKDIERSDLSPKLOSAPQODPAKYIE 180
Qy 181 MHVIVEKQLYNHMGSDTTVAQKVFOLIGLTNAIFVSNITIIISLLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQKVFOLIGLTNAIFVSNITIIISLLELWIDENKIATTG 240
Qy 241 EANELHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDDANYAGGVVLHPT 300
Db 241 EANELHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDDANYAGGVVLHPT 300
Qy 301 ISLESIAVILAQLLSLNGITYYDDINKCQCGAVCINMPEAIHFSGVKIFSNCSFEDFAH 360
Db 301 ISLESIAVILAQLLSLNGITYYDDINKCQCGAVCINMPEAIHFSGVKIFSNCSFEDFAH 360
Qy 361 FISKQKSOCLHNPRLDPPFKQAVCGNAKLEAGEECDCGTEQCDIATCRF 420
Db 361 FISKQKSOCLHNPRLDPPFKQAVCGNAKLEAGEECDCGTEQCDIATCRF 420
Qy 421 KAGSNCAEGPCENCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYYVOTGHPCGLNQ 480
Db 421 KAGSNCAEGPCENCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYYVOTGHPCGLNQ 480
Qy 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLI CKYVGFLLQI PRATIIYANISGHLICIAVEFASDHADSKQMWIKDGTSCGSKVC 600
Db 541 CGKLI CKYVGFLLQI PRATIIYANISGHLICIAVEFASDHADSKQMWIKDGTSCGSKVC 600
Qy 601 RNQRCVSSSYLYGYDCTTDKCNDRGVNCKKHCHCSASYLPDSCSVQSDLPWGGSIDSGNF 660
Db 601 RNQRCVSSSYLYGYDCTTDKCNDRGVNCKKHCHCSASYLPDSCSVQSDLPWGGSIDSGNF 660
Qy 661 PPVAIPARLPERRYENIYHSEKMPWPFLLFIPFFIIFCVLIAMVKNFORKKWRTEDY 720
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Db 721 SSDEQPESESEPKG 734
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RESULT 2

PCT-US95-07295-8

Sequence 8, Application PC/TUS9507295

GENERAL INFORMATION:

APPLICANT: ALVES, KENNETH

APPLICANT: GUPTA, SUNIL K.

APPLICANT: HOLLIS, GREGORY F.

TITLE OF INVENTION: CONTRACEPTIVE VACCINE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: MARY A. APPOLLINA

STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

CITY: RAYWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07295

FILING DATE:

CLASSIFICATION:

RESULT 3

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ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 734 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07295-8
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MWVLFLLSLGGLRMDNSFDSLPVQIITVPEKIRSIIEGIESQASYKIVIEGKPYTVNLM 60
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Db 61 QKNFLPHNFRVYSYSGTGIMKPLDQFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLQFE 120
Qy 121 NVSYGIEPLESSVGFHEVIYQVGHKADVSLYNEKDIERSDLSPKLOSAPQODPAKYIE 180
Db 121 NVSYGIEPLESSVGFHEVIYQVGHKADVSLYNEKDIERSDLSPKLOSAPQODPAKYIE 180
Qy 181 MHVIVEKQLYNHMGSDTTVAQKVFOLIGLTNAIFVSNITIIISLLELWIDENKIATTG 240
Db 181 MHVIVEKQLYNHMGSDTTVAQKVFOLIGLTNAIFVSNITIIISLLELWIDENKIATTG 240
Qy 241 EANELHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDDANYAGGVVLHPT 300
Db 241 EANELHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDDANYAGGVVLHPT 300
Qy 301 ISLESIAVILAQLLSLNGITYYDDINKCQCGAVCINMPEAIHFSGVKIFSNCSFEDFAH 360
Db 301 ISLESIAVILAQLLSLNGITYYDDINKCQCGAVCINMPEAIHFSGVKIFSNCSFEDFAH 360
Qy 361 FISKQKSOCLHNPRLDPPFKQAVCGNAKLEAGEECDCGTEQCDIATCRF 420
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Qy 421 KAGSNCAEGPCENCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYYVOTGHPCGLNQ 480
Db 421 KAGSNCAEGPCENCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYYVOTGHPCGLNQ 480
Qy 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMSGDQCTDTFGKEVEFGPSECSYSLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Qy 541 CGKLI CKYVGFLLQI PRATIIYANISGHLICIAVEFASDHADSKQMWIKDGTSCGSKVC 600
Db 541 CGKLI CKYVGFLLQI PRATIIYANISGHLICIAVEFASDHADSKQMWIKDGTSCGSKVC 600
Qy 601 RNQRCVSSSYLYGYDCTTDKCNDRGVNCKKHCHCSASYLPDSCSVQSDLPWGGSIDSGNF 660
Db 601 RNQRCVSSSYLYGYDCTTDKCNDRGVNCKKHCHCSASYLPDSCSVQSDLPWGGSIDSGNF 660
Qy 661 PPVAIPARLPERRYENIYHSEKMPWPFLLFIPFFIIFCVLIAMVKNFORKKWRTEDY 720
Db 661 PPVAIPARLPERRYENIYHSEKMPWPFLLFIPFFIIFCVLIAMVKNFORKKWRTEDY 720
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Db 721 SSDEQPESESEPKG 734
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US-08-264-101-2
; Sequence 2, Application US/08264101
; Patent No. 5693496
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAYWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,101
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-264-101-2

Query Match      88.6%; Score 650; DB 1; Length 651;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      145 KKADVSLYNEKDIESRDLSPKLSAEPQDFAKYIEMHVIKQYVHVEKQLYNHMGSDTTTVAQKV 204
DB      62 KKADVSLYNEKDIESRDLSPKLSAEPQDFAKYIEMHVIKQYVHVEKQLYNHMGSDTTTVAQKV 121
QY      205 FQILGLTNAIFVSNITIISSLELWIDENKIATTTGEANELLHTFLRWKTSYLVLRPHDV 264
DB      122 FQILGLTNAIFVSNITIISSLELWIDENKIATTTGEANELLHTFLRWKTSYLVLRPHDV 181
QY      265 AFLVVRKSNYVGCATFQGWKCDANYAGGVVLPRTISLESIAVILAQLLSLNGITYDD 324
DB      182 AFLVVRKSNYVGCATFQGWKCDANYAGGVVLPRTISLESIAVILAQLLSLNGITYDD 241
QY      325 INKQCQSGAVICINMPEAIHSGVKIFSNCSFEDFAHPIKQSKOCLHNQRLDPFFKQQA 384
DB      242 INKQCQSGAVICINMPEAIHSGVKIFSNCSFEDFAHPIKQSKOCLHNQRLDPFFKQQA 301
QY      385 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCNCLFMSKERM 444
DB      302 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCNCLFMSKERM 361
QY      445 RPSFECDLPEYCNCGSSASCPENHYVQTGHPGCLNQWICIDGVCMSGDCKCTDTFGKEVE 504
DB      362 RPSFECDLPEYCNCGSSASCPENHYVQTGHPGCLNQWICIDGVCMSGDCKCTDTFGKEVE 421

US-08-765-243-2
; Sequence 2, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAYWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-243-2

Query Match      88.6%; Score 650; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      85 QDFQNFCHYGYEGYKPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFHVIYQVKH 144
DB      2 QDFQNFCHYGYEGYKPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFHVIYQVKH 61
QY      145 KKADVSLYNEKDIESRDLSPKLSAEPQDFAKYIEMHVIKQYVHVEKQLYNHMGSDTTTVAQKV 204
DB      62 KKADVSLYNEKDIESRDLSPKLSAEPQDFAKYIEMHVIKQYVHVEKQLYNHMGSDTTTVAQKV 121
QY      205 FQILGLTNAIFVSNITIISSLELWIDENKIATTTGEANELLHTFLRWKTSYLVLRPHDV 264
DB      122 FQILGLTNAIFVSNITIISSLELWIDENKIATTTGEANELLHTFLRWKTSYLVLRPHDV 181
QY      265 AFLVVRKSNYVGCATFQGWKCDANYAGGVVLPRTISLESIAVILAQLLSLNGITYDD 324
DB      182 AFLVVRKSNYVGCATFQGWKCDANYAGGVVLPRTISLESIAVILAQLLSLNGITYDD 241
QY      325 INKQCQSGAVICINMPEAIHSGVKIFSNCSFEDFAHPIKQSKOCLHNQRLDPFFKQQA 384
DB      242 INKQCQSGAVICINMPEAIHSGVKIFSNCSFEDFAHPIKQSKOCLHNQRLDPFFKQQA 301
QY      385 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCNCLFMSKERM 444
DB      302 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCCNCLFMSKERM 361
QY      445 RPSFECDLPEYCNCGSSASCPENHYVQTGHPGCLNQWICIDGVCMSGDCKCTDTFGKEVE 504
DB      362 RPSFECDLPEYCNCGSSASCPENHYVQTGHPGCLNQWICIDGVCMSGDCKCTDTFGKEVE 421
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Db 122 FQIIGLTNAIFVSNITIISSLELWIDENKIATTGEANELLTFLRWKTSYLVLRPHDV 181
Qy 265 AFLVYREKSNYVGATFQGMKCDANYAGGVVHLHPTTISLESIAVILAQLLSLNGIYDD- 324
Db 182 AFLVYREKSNYVGATFQGMKCDANYAGGVVHLHPTTISLESIAVILAQLLSLNGIYDD 241
Qy 325 INKQCSCGAVCINMPEAIHFSGVKIFSNCSFEDFAHFISKQSOCLHNQPRLDPPFFKQA 384
Db 242 INKQCSCGAVCINMPEAIHFSGVKIFSNCSFEDFAHFISKQSOCLHNQPRLDPPFFKQA 301
Qy 385 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 444
Db 302 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 361
Qy 445 RPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQMICIDGVCMSGDKCTDTFGKEVE 504
Db 362 RPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQMICIDGVCMSGDKCTDTFGKEVE 421
Qy 505 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIQKYGKFLQIPRATTIYA 564
Db 422 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIQKYGKFLQIPRATTIYA 481
Qy 565 NISGHLCIAVEFASDHADSQMWIKDGTSCGSKNVCNQRQCVSSSYLGDCYDCTDKCNDRG 624
Db 482 NISGHLCIAVEFASDHADSQMWIKDGTSCGSKNVCNQRQCVSSSYLGDCYDCTDKCNDRG 541
Qy 625 VCNKXKHCHCSASYLPDSCVSQDLWPGGSDSGNFKVCRNQRQCVSSSYLGDCYDCTDKCNDRG 684
Db 542 VCNKXKHCHCSASYLPDSCVSQDLWPGGSDSGNFKVCRNQRQCVSSSYLGDCYDCTDKCNDRG 601
Qy 685 RWPFFLPIFPFIIFCVLIAIMVKVNFQKWKRTEDYSSDQSESEPKG 734
Db 602 RWPFFLPIFPFIIFCVLIAIMVKVNFQKWKRTEDYSSDQSESEPKG 651

RESULT 5
PCT-US95-07295-2
; Sequence 2, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLISS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
PCT-US95-07295-2
Query Match 88.6%; Score 650; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 650; Conservative 0; Mismatches 0; Indels- 0; Gaps 0;

Qy 85 QDFQNFCHQGYEGYKPKSVVMYSTCTGLRGVLQFENVSYGIEPLLESSVGFHVIYQVKH 144
Db 2 QDFQNFCHQGYEGYKPKSVVMYSTCTGLRGVLQFENVSYGIEPLLESSVGFHVIYQVKH 61
Qy 145 KKADVSLYNEKDIESRDLSPKLSABPQDFAKYIEKHVIVEKQLYNHNMGSDTTVAQKV 204
Db 62 KKADVSLYNEKDIESRDLSPKLSABPQDFAKYIEKHVIVEKQLYNHNMGSDTTVAQKV 121
Qy 205 FQIIGLTNAIFVSNITIISSLELWIDENKIATTGEANELLTFLRWKTSYLVLRPHDV 264
Db 122 FQIIGLTNAIFVSNITIISSLELWIDENKIATTGEANELLTFLRWKTSYLVLRPHDV 181
Qy 265 AFLVYREKSNYVGATFQGMKCDANYAGGVVHLHPTTISLESIAVILAQLLSLNGIYDD 324
Db 182 AFLVYREKSNYVGATFQGMKCDANYAGGVVHLHPTTISLESIAVILAQLLSLNGIYDD 241
Qy 325 INKQCSCGAVCINMPEAIHFSGVKIFSNCSFEDFAHFISKQSOCLHNQPRLDPPFFKQA 384
Db 242 INKQCSCGAVCINMPEAIHFSGVKIFSNCSFEDFAHFISKQSOCLHNQPRLDPPFFKQA 301
Qy 385 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 444
Db 302 VCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 361
Qy 445 RPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQMICIDGVCMSGDKCTDTFGKEVE 504
Db 362 RPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQMICIDGVCMSGDKCTDTFGKEVE 421
Qy 505 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIQKYGKFLQIPRATTIYA 564
Db 422 FGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLIQKYGKFLQIPRATTIYA 481
Qy 565 NISGHLCIAVEFASDHADSQMWIKDGTSCGSKNVCNQRQCVSSSYLGDCYDCTDKCNDRG 624
Db 482 NISGHLCIAVEFASDHADSQMWIKDGTSCGSKNVCNQRQCVSSSYLGDCYDCTDKCNDRG 541
Qy 625 VCNKXKHCHCSASYLPDSCVSQDLWPGGSDSGNFKVCRNQRQCVSSSYLGDCYDCTDKCNDRG 684
Db 542 VCNKXKHCHCSASYLPDSCVSQDLWPGGSDSGNFKVCRNQRQCVSSSYLGDCYDCTDKCNDRG 601
Qy 685 RWPFFLPIFPFIIFCVLIAIMVKVNFQKWKRTEDYSSDQSESEPKG 734
Db 602 RWPFFLPIFPFIIFCVLIAIMVKVNFQKWKRTEDYSSDQSESEPKG 651

RESULT 6
US-10-000-489-70
; Sequence 70, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
```

PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Jpatent
; SEQ ID NO 70
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..16
US-10-000-489-70

Query Match 2.0%; Score 15; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LQFENVSYGIEPLES 131
Db 121 LQFENVSYGIEPLES 135

RESULT 7
PCT-US93-05640-34
; Sequence 34, Application PC/TUS9305640
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05640
; FILING DATE: 19930610
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/897,883
; FILING DATE: June 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UCT90-01AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-05640-34

Query Match 1.6%; Score 12; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 605 CVSSSYLGVDCT 616
Db 33 CVSSSYLGVDCT 44

RESULT 8
PCT-US93-05640-16
; Sequence 16, Application PC/TUS9305640
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05640
; FILING DATE: 19930610
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/897,883
; FILING DATE: June 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UCT90-01AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-05640-16

Query Match 1.8%; Score 12; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 ECDLPEYCNCGSS 461
Db 26 ECDLPEYCNCGSS 37

RESULT 9
PCT-US93-05640-25
; Sequence 25, Application PC/TUS9305640
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05640
; FILING DATE: 19930610

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/897,883
; FILING DATE: June 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UCT90-01AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-05640-25

Query Match 1.6%; Score 12; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 ECDLPEYCGSS 461
Db 26 ECDLPEYCGSS 37

RESULT 10
US-08-765-243-6
; Sequence 6, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-243-6

Query Match 1.6%; Score 12; DB 2; Length 735;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US95-07295-6
; Sequence 6, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07295-6

Query Match 1.6%; Score 12; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 NVSYGIEPLESS 132
Db 128 NVSYGIEPLESS 139

RESULT 11
PCT-US95-07295-6
; Sequence 6, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07295-6

Query Match 1.6%; Score 12; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 NVSYGIEPLESS 132
Db 128 NVSYGIEPLESS 139

RESULT 12
PCT-US93-05640-12
; Sequence 12, Application PC/TUS9305640
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05640
; FILING DATE: 19930610
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/897,883
; FILING DATE: June 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UCT90-01AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-05640-12

Query Match 1.4%; Score 10; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 LEAGEECDCG 400
Db 10 LEAGEECDCG 19

RESULT 13
PCT-US93-05640-23
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05640
; FILING DATE: 19930610
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/897,883
; FILING DATE: June 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UCT90-01AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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PCT-US93-05640-23

Query Match 1.4%; Score 10; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 LEAGEECDCG 400
Db 10 LEAGEECDCG 19

RESULT 14
US-08-993-165-16
; Sequence 16, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yunqiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
US-08-993-165-16

Query Match 1.4%; Score 10; DB 3; Length 68;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EAGEECDCGT 401
Db 1 EAGEECDCGT 10

RESULT 15
US-09-540-448-16
; Sequence 16, Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
US-09-540-448-16

Query Match 1.4%; Score 10; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EAGEECDCGT 401
Db 1 EAGEECDCGT 10
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Search completed: January 10, 2005, 22:39:42

Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 22:28:38 ; Search time 44 Seconds
(without alignments)
1605.071 Million cell updates/sec

Title: US-10-054-683-19
Perfect score: 734
Sequence: 1 MVLVLLSLGLGRLMDSNFD.....WRTDYSSDEQPESEPKG 734

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734	100.0	734	2	JC4861
2	52	7.1	735	2	fertilin beta cha
3	12	1.6	357	2	sperm surface prot
4	10	1.4	71	2	batroxostatin - ba
5	10	1.4	73	2	platelet aggregati
6	10	1.4	73	2	platelet aggregati
7	10	1.4	416	2	hemorrhagic protei
8	10	1.4	481	2	fibrinolytic prote
9	10	1.4	812	2	truncin precursor
10	10	1.4	736	2	tMDC 1 protein - c
11	9	1.2	71	2	KGD-bearing platel
12	9	1.2	71	2	aplaggin - easter
13	9	1.2	72	2	platelet aggregati
14	9	1.2	72	2	platelet aggregati
15	9	1.2	73	2	platelet aggregati
16	9	1.2	73	2	platelet aggregati
17	9	1.2	73	2	platelet aggregati
18	9	1.2	73	2	platelet aggregati
19	9	1.2	73	2	platelet aggregati
20	9	1.2	524	2	disintegrin-like m
21	9	1.2	655	2	disintegrin and me
22	9	1.2	660	2	metalloproteinase
23	9	1.2	670	2	disintegrin-like m
24	9	1.2	671	2	probable membrane
25	9	1.2	823	2	cyttestin precurs
26	8	1.1	71	2	platelet aggregati
27	8	1.1	72	2	platelet aggregati
28	8	1.1	72	2	platelet aggregati
29	8	1.1	72	2	platelet aggregati

30	8	1.1	151	2	S60259	meltrin gamma - mo
31	8	1.1	151	2	A69227	hypothetical prote
32	8	1.1	233	2	A72786	probable transport
33	8	1.1	394	2	B64696	hypothetical prote
34	8	1.1	417	2	A64573	hypothetical prote
35	8	1.1	419	2	A59414	metalloproteinase
36	8	1.1	526	2	B75202	d-aminocyclase (as
37	8	1.1	549	2	S48169	metalloproteinase
38	8	1.1	571	2	S24789	jararhagin C precu
39	8	1.1	609	2	S55270	catrocollastatin p
40	8	1.1	777	2	I48100	ADAM 5 protein pre
41	8	1.1	825	2	S55060	fertilin alpha-II
42	8	1.1	905	2	S55059	fertilin alpha-I -
43	7	1.0	59	2	C71684	hypothetical prote
44	7	1.0	60	2	J50583	hypothetical 7K pr
45	7	1.0	61	1	N1NJ1B	short neurotoxin 1

ALIGNMENTS

RESULT 1

JC4861
fertilin beta chain - human
C/Species: Homo sapiens (man)
C/Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C/Accession: JC4861
R/Gupta, S.K.; Alves, K.; O'Neill Palladin, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A/Title: Molecular cloning of the human fertilin beta subunit.
A/Reference number: JC4861; MUID:96295488; PMID:8702389
A/Accession: JC4861
A/Molecule type: mRNA
A/Residues: 1-734 <GUP>
A/Cross-references: UNIPROT:Q99965; GB:U38805; NID:G4151118; PIDN:RAD04206.1; PID:G41511
C/Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C/Superfamily: mouse meltrin alpha; disintegrin homology
C/Keywords: glycoprotein; integrin binding; transmembrane protein
F/382-734/Product: fertilin beta chain #status predicted <NAT>
F/382-467/Domain: disintegrin homology <DIS>
F/448-450/Region: integrin binding #status predicted
F/686-708/Domain: transmembrane #status predicted <TM>
F/121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match		100.0%	Score	734	DB 2	Length	734
Best Local Similarity		100.0%	Pred. No.	0			
Matches		734	Conservative	0	Mismatches	0	Gaps
0							
Qy	1	MVLVLLSLGLGRLMDSNFD	SLPVQITVPKIRSI	KEGIESQASYKIVIEGKPYTNLM	60		
Db	1	MVLVLLSLGLGRLMDSNFD	SLPVQITVPKIRSI	KEGIESQASYKIVIEGKPYTNLM	60		
Qy	61	QKNFLPHNFRVYSYSGTGMKPLDDQFQNFCHYGVYKPSVMVSTCTGLRGVLQFE	120				
Db	61	QKNFLPHNFRVYSYSGTGMKPLDDQFQNFCHYGVYKPSVMVSTCTGLRGVLQFE	120				
Qy	121	NVSYGIEPLESSVGFHVIYQVKKADVSLYNEKDI	ESRDLSPKLSAQSPQDFAKYIE	180			
Db	121	NVSYGIEPLESSVGFHVIYQVKKADVSLYNEKDI	ESRDLSPKLSAQSPQDFAKYIE	180			
Qy	181	MHVIVEKQLYNNHMGSDTTVAQVQLIGLTNAIFVSFNIT	ILSSLELWIDENKIATTG	240			
Db	181	MHVIVEKQLYNNHMGSDTTVAQVQLIGLTNAIFVSFNIT	ILSSLELWIDENKIATTG	240			
Qy	241	EANELHHTFLRWKTSYLVLPHDVAFLVYREKSNYVGFQGMKCDANVAGGVVLPRT	300				
Db	241	EANELHHTFLRWKTSYLVLPHDVAFLVYREKSNYVGFQGMKCDANVAGGVVLPRT	300				
Qy	301	ISLESIAVILAQLLSLSMGITYDDINKCQCSGAVCMNPEAIHFSVGKIFSNCSFEDFAH	360				
Db	301	ISLESIAVILAQLLSLSMGITYDDINKCQCSGAVCMNPEAIHFSVGKIFSNCSFEDFAH	360				
Qy	361	FISKQKSCQLHNPRLDPFPFKQAQVCGNAKLEAGEBCDCTEQDCALIGETCCDIATCRF	420				

Db 361 FISQKSOCLHNPRLDPFFRQQAQVGNKALEAGEEDCGTEQDCALIGETCCDIATCRF 420
Qy 421 KAGNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQ 480
Db 421 KAGNCAEGPCCNCLFMSKERMCRPSFECDLPEYCNCGSSASCENHYVOTGHPGCLNQ 480
Qy 481 WICIDGVCMGSDKQCTDTFGKEVFGFSECYSHLNSKTDVSGNGCISDSGYTQCEADNLQ 540
Db 481 WICIDGVCMGSDKQCTDTFGKEVFGFSECYSHLNSKTDVSGNGCISDSGYTQCEADNLQ 540
Qy 541 CGKLICKYVGFLLQIPRATIIYANISGHLICIAVEFASDHADSKQMKIKDGTSCGSKNVC 600
Db 541 CGKLICKYVGFLLQIPRATIIYANISGHLICIAVEFASDHADSKQMKIKDGTSCGSKNVC 600
Qy 601 RNORCVSSYLGXDCTTDKNDRGVGNKXKCHCSASVLPDCSVQSDLPFGGSDSGNF 660
Db 601 RNORCVSSYLGXDCTTDKNDRGVGNKXKCHCSASVLPDCSVQSDLPFGGSDSGNF 660
Qy 661 PPVAIPARLPERRIENIYHSKPMRPFLLFIPFFIIFCVLIAMVKNVFORKKWRTEDY 720
Db 661 PPVAIPARLPERRIENIYHSKPMRPFLLFIPFFIIFCVLIAMVKNVFORKKWRTEDY 720
Qy 721 SSDEQPSSESPKG 734
Db 721 SSDEQPSSESPKG 734

RESULT 2
G02937
fertilin beta - crab-eating macaque
C/Species: Macaca fascicularis (Crab-eating macaque)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C/Accession: G02937; S55061
R/Ramarao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
submitted to the EMBL Data Library, August 1995
A/Reference number: G12615
A/Accession: G02937
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-735 <RAM>
A/Cross-references: UNIPROT:Q28478; EMBL:U03959; NID:G998339; PID:G998340
R/Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A/Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.
A/Reference number: S55059; MUID:95260313; PMID:7741716
A/Accession: S55061
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-722, 'S', 724-735 <PER>
A/Cross-references: EMBL:X77653; NID:G794076; PIDN:CAA54733.1; PID:G794077
C/Species: mouse meltrin alpha; disintegrin homology
F/393-468/Domain: disintegrin homology <DIS>

Query Match 7.1%; Score 52; DB 2; Length 735;
Best Local Similarity 100.0%; Pred. No. 7.6e-46;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LOFENVSYGIEPLESSVGFHVIYQVKKADVSLYNEKDIERSDLSPKLOS 168
Db 118 LOFENVSYGIEPLESSVGFHVIYQVKKADVSLYNEKDIERSDLSPKLOS 169

RESULT 3
S23403
sperm surface protein PH-30 beta chain precursor - guinea pig (fragment)
C/Species: Cavia porcellus (guinea pig)
C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jun-2000
C/Accession: S23403; S25696
R/Blobel, C.P.; Wolfberg, T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
Nature 356, 248-252, 1992
A/Title: A potential fusion peptide and an integrin ligand domain in a protein active in
A/Reference number: S23402; MUID:92204234; PMID:1552944

A/Accession: S23403
A/Molecule type: mRNA
A/Residues: 1-357 <BL01>
A/Cross-references: EMBL:Z11720
A/Accession: S25696
A/Molecule type: protein
A/Residues: 5-8, 'X', 10-32; 67-88; 125-129, 'X', 131-134, 'X', 136-141, 'X', 143; 154, 'X', 156-161;
C/Species: mouse meltrin alpha; disintegrin homology
C/Keywords: glycoprotein; transmembrane protein
F/1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F/5-357/Product: sperm surface protein PH-30 beta chain #status experimental <MAT>
F/5-87/Domain: disintegrin homology <DIS>
F/303-323/Domain: transmembrane #status predicted <TM>
F/78,186,256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.6%; Score 12; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 ECDLPEYCNCGSS 461
Db 70 ECDLPEYCNCGSS 81

RESULT 4
S13168
batroxostatin - barba amarilla
C/Species: Bothrops atrox (barba amarilla, fer-de-lance)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C/Accession: S13168
R/Rucinski, B.; Niewiarowski, S.; Holt, J.C.; Soszka, T.; Knudsen, K.A.
Biochim. Biophys. Acta 1054, 257-262, 1990
A/Title: Batroxostatin, an Arg-Gly-Asp-containing peptide from Bothrops atrox, is a potent
A/Reference number: S13168; MUID:91002685; PMID:2207176
A/Accession: S13168
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-71 <RUC>
A/Cross-references: UNIPROT:P18618
C/Species: disintegrin homology
F/1-69/Domain: disintegrin homology (fragment) <DIS>
F/51-53/Region: cell attachment (R-G-D) motif

Query Match 1.4%; Score 10; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 392 EAGECDCCGT 401
Db 1 EAGECDCCGT 10

RESULT 5
A43020
platelet aggregation disintegrin (jararacin), venom - jararacussu
C/Species: Bothrops jararacussu (jararacussu)
C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 10-Jul-1998
C/Accession: A43020
R/Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J.
J. Biol. Chem. 268, 1058-1065, 1993
A/Title: Characterization of the integrin specificities of disintegrins isolated from Ame-
A/Reference number: A43019; MUID:93123215; PMID:8419314
A/Accession: A43020
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-73 <SCA>
C/Species: unassigned disintegrins; disintegrin homology
F/3-69/Domain: disintegrin homology <DIS>

Query Match 1.4%; Score 10; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EAGEECDCGT 401
|||||
Db 1 EAGEECDCGT 10

RESULT 6

A43019
platelet aggregation disintegrin (cerastin), venom - Mojave Desert sidewinder
C/Species: Crotalus cerastes cerastes (Mojave Desert sidewinder)
C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C/Accession: A43019
R/Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993
A/Title: Characterization of the integrin specificities of disintegrins isolated from Am
A/Reference number: A43019; MUID:93123215; PMID:8419314
A/Accession: A43019
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-73 <SCA>
A/Cross-references: UNIPROT:P31982
C/Superfamily: unassigned disintegrins; disintegrin homology
F;1-69/Domain: disintegrin homology (fragment) <Dis>

Query Match 1.4%; Score 10; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 EAGEECDCGT 401
|||||
Db 1 EAGEECDCGT 10

RESULT 7

A37877
hemorrhagic protein HR1B - habu
C/Species: Trimeresurus flavoviridis (habu)
C/Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C/Accession: A37877
R/Takeya, H.; Oda, K.; Miyata, T.; Omori-Sato, T.; Iwanaga, S.
J. Biol. Chem. 265, 16068-16073, 1990
A/Title: The complete amino acid sequence of the high molecular mass hemorrhagic protein
A/Reference number: A37877; MUID:90375459; PMID:2398046
A/Accession: A37877
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-416 <TAK>
A/Cross-references: UNIPROT:P20164
C/Superfamily: mouse meltrin alpha: disintegrin homology
F;210-292/Domain: disintegrin homology <Dis>
F;144/Active site: Glu #status predicted

Query Match 1.4%; Score 10; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 LEAGEECDCG 400
|||||
Db 219 LEAGEECDCG 228

RESULT 8

JC4342
fibrinolytic proteinase (EC 3.4.24.-) precursor - Chinese habu
N/Alternate names: fibrinogenolytic proteinase
C/Species: Trimeresurus mucrosquamatus (Chinese habu)
C/Date: 21-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C/Accession: JC4342; PC4108
R/Huang, K.F.; Hung, C.C.; Pan, F.M.; Chow, L.P.; Tsugita, A.; Chiou, S.H.
Biochem. Biophys. Res. Commun. 216, 223-233, 1995
A/Title: Characterization of multiple metalloproteinases with fibrinogenolytic activity
analysis.
A/Reference number: JC4342; MUID:96067555; PMID:7488093
A/Accession: JC4342

A/Molecule type: mRNA
A/Residues: 1-481 <HUA>
A/Cross-references: UNIPROT:Q92119; EMBL:X91190
A/Accession: PC4108
A/Molecule type: protein
A/Residues: 237-251 <HU2>
A/Experimental source: venom gland
C/Comment: The proteolytic activity is inhibited by EDTA or phenanthroline.
C/Superfamily: trigramin precursor; disintegrin homology
C/Keywords: anticoagulant; hydrolase; metalloproteinase; venom; zinc
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-187/Domain: propeptide #status predicted <PRO>
F;188-392/Product: fibrinolytic proteinase #status predicted <MAT>
F;399-477/Domain: disintegrin homology <Dis>
F;411-478/Product: disintegrin #status predicted <DNT>
F;459-461/Region: cell attachment (R-G-D) motif
F;333,337,343/Binding site: zinc, catalytic (His) #status predicted
F;334/Active site: Glu #status predicted

Query Match 1.4%; Score 10; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 LEAGEECDCG 400
|||||
Db 408 LEAGEECDCG 417

RESULT 9

S43125
trimucin precursor - Chinese habu
N/Contains: hemorrhagic proteinase (EC 3.4.24.-); platelet aggregation inhibitor (disint
C/Species: Trimeresurus mucrosquamatus (Chinese habu)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S47570; S43125
R/Tsai, I.H.; Wang, Y.M.; Lee, Y.H.
Biochim. Biophys. Acta 1200, 337-340, 1994
A/Title: Characterization of a cDNA encoding the precursor of platelet aggregation inhibi
A/Reference number: S47570; MUID:94347824; PMID:8068721
A/Accession: S47570
A/Molecule type: mRNA
A/Residues: 1-481 <TS2>
A/Cross-references: UNIPROT:Q91505; EMBL:X77089; MID:9467703; PIDN:CAAS4364.1; PID:94677
C/Superfamily: trigramin precursor; disintegrin homology
C/Keywords: anticoagulant; hydrolase; metalloproteinase; venom; zinc
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-187/Domain: propeptide #status predicted <PRO>
F;188-392/Product: hemorrhagic proteinase #status predicted <HEM>
F;399-477/Domain: disintegrin homology <Dis>
F;411-478/Product: disintegrin #status predicted <DNT>
F;459-461/Region: cell attachment (R-G-D) motif
F;333,337,343/Binding site: zinc, catalytic (His) #status predicted
F;334/Active site: Glu #status predicted

Query Match 1.4%; Score 10; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 LEAGEECDCG 400
|||||
Db 408 LEAGEECDCG 417

RESULT 10

S47645
tMDC 1 protein - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C/Accession: S47645
R/Barker, H.L.; Perry, A.C.F.; Jones, R.; Hall, L.
Biochim. Biophys. Acta 1218, 429-431, 1994
A/Title: Sequence and expression of a monkey testicular transcript encoding tMDC 1, a no
A/Reference number: S47645; MUID:94325353; PMID:8049267

A;Accession: S47645
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-736 <BAR>
A;Cross-references: UNIPROT:Q28482; EMBL:X76637; NID:g535016; PIDN:CAA54085.1; PID:g535016
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;392-477/Domain: disintegrin homology <DIS>

Query Match 1.4%; Score 10; DB 2; Length 736;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 123 SYGIEPLESS 132
Db 127 SYGIEPLESS 136

RESULT 11
A59412
KGD-bearing platelet-aggregation disintegrin (ussuristatin) 2 - Agkistrodon ussuriensis
C;Species: Agkistrodon ussuriensis
C;Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004
C;Accession: A59412
R;Terada, S.
J. Biochem. 125, 31-35, 1999
A;Title: Ussuristatin 2, A Novel KGD-Bearing Disintegrin from Agkistrodon ussuriensis
A;Reference number: A59412
A;Accession: A59412
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-71 <TER>
A;Cross-references: UNIPROT:Q7LZT4
C;Keywords: anticoagulant; integrin inhibitor; venom

Query Match 1.2%; Score 9; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 392 EAGEECDCG 400
Db 1 EAGEECDCG 9

RESULT 12
A33990
aplaggin - eastern cottonmouth
C;Species: Agkistrodon piscivorus piscivorus (eastern cottonmouth)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33990
R;Chao, B.H.; Jakubowski, J.A.; Savage, B.; Chow, E.P.; Marzec, U.M.; Harker, L.A.; Mara
Proc. Natl. Acad. Sci. U.S.A. 86, 8050-8054, 1989
A;Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a potent inhi
A;Reference number: A33990; MUID:90046735; PMID:2510158
A;Accession: A33990
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-71 <CHA>
A;Cross-references: UNIPROT:P16338
C;Superfamily: unassigned disintegrins; disintegrin homology
F;1-68/Domain: disintegrin homology (fragment) <DIS>

Query Match 1.2%; Score 9; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 392 EAGEECDCG 400
Db 1 EAGEECDCG 9

RESULT 13
F43019
platelet aggregation disintegrin (cotlarin), venom - cotiara

C;Species: Bothrops cotiara (cotiara)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004
C;Accession: F43019
R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J.
J. Biol. Chem. 268, 1058-1065, 1993
A;Title: Characterization of the integrin specificities of disintegrins isolated from Am
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;392-477/Domain: disintegrin homology (fragment) <DIS>

Query Match 1.2%; Score 9; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 392 EAGEECDCG 400
Db 1 EAGEECDCG 9

RESULT 14
B43020
platelet aggregation disintegrin (cereberin), venom - Arizona black rattlesnake
C;Species: Crotalus viridis cerberus (Arizona black rattlesnake)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C;Accession: B43020
R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J.
J. Biol. Chem. 268, 1058-1065, 1993
A;Title: Characterization of the integrin specificities of disintegrins isolated from Am
A;Reference number: A43019; MUID:93123215; PMID:8419314
A;Accession: B43020
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-72 <SCA>
A;Cross-references: UNIPROT:P31985
C;Superfamily: unassigned disintegrins; disintegrin homology
F;3-69/Domain: disintegrin homology <DIS>

Query Match 1.2%; Score 9; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 392 EAGEECDCG 400
Db 1 EAGEECDCG 9

RESULT 15
A59410
platelet aggregation disintegrin (brevicaudin) 1b, venom - Gloydius halys brevicaud
C;Species: Gloydius halys brevicaud
C;Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004
C;Accession: A59410
R;Terada, S.
Fukuoka Univ. Sci. Reports 30, 71-78, 2000
A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloydi
A;Reference number: A59409
A;Accession: A59410
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-73 <TER>
A;Cross-references: UNIPROT:Q90220
C;Keywords: anticoagulant; integrin inhibitor; venom

Query Match 1.2%; Score 9; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 392 EAGEECDCG 400

Db |||||||
 1 EAGECDG 9

Search completed: January 10, 2005, 22:38:56
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 22:27:53 ; Search time 202 Seconds
(without alignments)
2090.718 Million cell updates/sec

Title: US-10-054-683-19
Perfect score: 734
Sequence: 1 MWVFLSLGLGLRMDNSFD.....WRTDYSSDEQPESEPKG 734

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	631	86.0	735	1	AD02_HUMAN	Q9965 homo sapien
2	241	32.8	579	2	Q6P2G0	Q6P290 homo sapien
3	241	32.8	579	2	AAH64547	AAH64547 homo sapi
4	52	7.1	735	1	AD02_MACFA	Q28478 macaca fasc
5	20	2.7	735	2	Q86588	Q86588 sus scrofa
6	20	2.7	731	1	AD02_RABIT	Q28660 oryctolagus
7	18	2.5	735	1	AD02_CAVPO	Q60411 cavia porce
8	16	2.2	746	1	AD18_MACFA	Q95194 macaca fasc
9	15	2.0	279	2	Q6ZWL1	Q6ZWL1 homo sapien
10	15	2.0	279	2	BAC85489	BAC85489 homo sapi
11	15	2.0	787	2	Q8TC27	Q8TC27 homo sapien
12	15	2.0	787	2	Q8TC42	Q8TC42 homo sapien
13	15	2.0	787	2	AAQ89099	AAQ89099 homo sapi
14	14	1.9	745	1	AD02_BOVIN	Q77780 bos taurus
15	13	1.8	677	2	Q8BJ80	Q8BJ80 mus musculu
16	13	1.8	719	1	AD18_MOUSE	Q9157 mus musculu
17	13	1.8	730	2	Q80Y08	Q80Y08 mus musculu
18	13	1.8	737	1	AD02_RAT	Q83202 rattus norv
19	13	1.8	750	2	Q6P901	Q6P901 mus musculu
20	13	1.8	750	2	Q8K410	Q8K410 mus musculu
21	13	1.8	750	2	AAH60983	AAH60983 mus muscu
22	12	1.6	735	1	AD02_MOUSE	Q50718 mus musculu
23	12	1.6	873	2	Q42595	Q42595 xenopus lae
24	11	1.5	77	2	Q80124	Q80124 bothrops al
25	11	1.5	474	2	Q95LW7	Q95LW7 macaca fasc
26	10	1.4	71	1	DIS1_BOTAT	P18618 bothrops at
27	10	1.4	73	1	DIS1_BOTJA	P31989 bothrops ja
28	10	1.4	73	1	DIS1_CROCC	P31982 crotalus ce
29	10	1.4	105	2	Q78CF2	Q78CF2 agkistrodon
30	10	1.4	317	2	Q90WC0	Q90WC0 agkistrodon
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RESULT 1

ID	AD02_HUMAN	STANDARD;	PRT;	735 AA.
DT	Q99955; P78326; Q9UQ08;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)			
DE	(Fertilin beta subunit) (PH-30) (PH30).			
GN	Name=ADAM2; Synonyms=FTNB;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
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RC	TISSUE=Testis;			
RX	MEDLINE=97193554; PubMed=9041139;			
RA	Vidaeus C.M., von Kap-Herr C., Golden W.L., Eddy R.L., Shows T.B.,			
RA	Herr J.C.;			
RT	"Human fertilin beta: identification, characterization, and			
RT	chromosomal mapping of an ADAM gene family member.";			
RL	Mol. Reprod. Dev. 46:363-369(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Testis;			
RX	MEDLINE=96295488; PubMed=8702389;			
RA	Gupta S.K., Alves K., Palladino L.O., Mark G.E., Hollis G.F.;			
RT	"Molecular cloning of the human fertilin beta subunit.";			
RL	Biochem. Biophys. Res. Commun. 224:318-326(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Testis;			
RX	MEDLINE=97224507; PubMed=9070941;			
RA	Burkin H.R., Burkin D.J., Davey P.M., Griffin D.K., Affara N.A.;			
RT	"Mapping, sequence, and expression analysis of the human fertilin beta			
RT	gene (FTNB).";			
RL	Genomics 40:190-192(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Testis;			
RA	Hall L., Frayne J.;			
RT	"Nucleotide sequence of the human fertilin beta transcript.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Testis;			
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			

P14530 trimereauru
Q90220 agkistrodon
Q72269 trimereauru
O57413 trimereauru
Q90YA7 trimereauru
Q91505 trimereauru
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F18619 trimereauru
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O73795 agkistrodon
Q8J1R1 trimereauru
Q7Q104 anopheles g
Q28482 macaca fasc
Q6TY20 mus musculu

ALIGNMENTS

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Johnson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krawczynski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Sperm surface membrane protein that may be involved in
CC sperm-egg plasma membrane adhesion and fusion during
CC fertilization. Could have a direct role in sperm-zona binding or
CC migration of sperm from the uterus into the oviduct. Interactions
CC with egg membrane could be mediated via binding between its
CC disintegrin-like domain to one or more integrins receptors on the
CC egg. This is a non catalytic metalloprotease-like protein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q99965-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q99965-2; Sequence=VSP_005471;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expressed specifically in spermatogenic cells
CC in the seminiferous cells. Not detected in fetal tissues.
CC -1- DOMAIN: A tripeptide motif (FEE) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding.
CC -1- PTM: The prodomain and the metalloprotease domain are cleaved
CC during the epididymal maturation of the spermatozoa.
CC -1- MISCELLANEOUS: In mammals, exists as a heterodimer composed of an
CC alpha and beta subunits. In human, fertilin alpha is a pseudogene.
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U52370; AAC51110.1; -;
CC EMBL; U38805; RAD04206.1; -;
CC EMBL; X99374; CAAG7753.1; -;
CC EMBL; AJ133005; CAB40813.1; -;
CC EMBL; BC034957; AAB34957.1; -;
CC PIR; JC4861; JC4861.
CC HSP; P30403; IN4Y.
CC MEROPS; M12_950; -;
CC Genew; HGNC:198; ADAM2.
CC MIM; 601533; -;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005178; F: integrin binding; TAS.
CC GO; GO:0008237; F: metalloprotease activity; TAS.
CC GO; GO:0007342; P: fusion of sperm to egg plasma membrane; TAS.
CC InterPro; IPR006586; ADAM_cysteine.
CC InterPro; IPR001762; Disintegrin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR001590; Peptidase M12B.
CC InterPro; IPR002870; Peptidase M12B_N.
CC InterPro; IPR006025; Pept_M_2n_BS.
CC Pfam; PF00200; Disintegrin_1;
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CC Pfam; PF01421; Reprolysin; 1.

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DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SMO0608; ACR; 1.
DR SMART; SMO0050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
KW Alternative splicing; Cell adhesion; EGF-like domain; Glycoprotein;
KW Signal; Transmembrane.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 174
FT CHAIN 175 735 ADAM 2.
FT DOMAIN 175 686 Extracellular (Potential).
FT TRANSMEM 687 707 Potential.
FT DOMAIN 708 735 Cytoplasmic (Potential).
FT DOMAIN 175 382 Metalloprotease-like.
FT DOMAIN 383 475 Disintegrin-like.
FT DOMAIN 477 606 Cys-rich.
FT DOMAIN 612 645 EGF-like.
FT DISULFID 287 370 By similarity.
FT DISULFID 329 354 By similarity.
FT DISULFID 445 458 Potential.
FT DISULFID 616 627 By similarity.
FT DISULFID 621 633 By similarity.
FT DISULFID 635 644 By similarity.
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 459 459 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 566 566 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 172 190 Missing (in isoform 2).
FT FTId=VSP_005471.
FT CONFLICT 3 3 Missing (in Ref. 2).
FT CONFLICT 21 21 D -> H (in Ref. 3).
FT CONFLICT 99 99 E -> D (in Ref. 3).
FT CONFLICT 106 106 V -> G (in Ref. 3).
FT CONFLICT 170 170 V -> A (in Ref. 2).
FT CONFLICT 288 288 D -> H (in Ref. 1).
FT CONFLICT 321 321 I -> T (in Ref. 1).
FT CONFLICT 388 388 G -> S (in Ref. 3).
FT CONFLICT 396 398 EEC -> DEF (in Ref. 3).
FT CONFLICT 501 501 G -> S (in Ref. 3).
FT CONFLICT 529 529 D -> V (in Ref. 3).
FT CONFLICT 579 579 S -> G (in Ref. 3).
FT CONFLICT 588 588 W -> L (in Ref. 3).
FT CONFLICT 603 603 N -> D (in Ref. 3).
FT CONFLICT 629 630 NK -> KQ (in Ref. 3).
FT CONFLICT 638 638 S -> F (in Ref. 3).
SQ SEQUENCE 735 AA; 82456 MW; 92867B5340BEE01F CRC64;
Query Match 86.0%; Score 631; DB 1; Length 735;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 VLFLLSGLGLRMDSNFDSLPVOITVPEKRSIIKEGIESQASQYKIVIEGKPYTNLMQK 62
DB 4 VLFLLSGLGLRMDSNFDSLPVOITVPEKRSIIKEGIESQASQYKIVIEGKPYTNLMQK 63
QY 63 NPLPHFRVYSYSGTGIMKFLDQDFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLPENY 122
DB 64 NPLPHFRVYSYSGTGIMKFLDQDFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLPENY 123
QY 123 SYGIEPLESSVGFEHYIYQVKKHKADVSLNEXKDIESRDLSPFKLSAEPQDFAKYIEMH 182
DB 124 SYGIEPLESSVGFEHYIYQVKKHKADVSLNEXKDIESRDLSPFKLSAEPQDFAKYIEMH 183
QY 183 VIVEKQLYNHMGSDTTVAQKVFQILGLTNVAFVSNFTIILSSLEWIDENKIATGEEA 242
DB 184 VIVEKQLYNHMGSDTTVAQKVFQILGLTNVAFVSNFTIILSSLEWIDENKIATGEEA 243
QY 243 NELLHTFLRWKTSYLVLRPHDVAFLVLYREKSNVYGATFGKMCNDANYAGGVVHLHPTIS 302

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Db 244 NELLHTFLRWKTSVLRLPHDVAELLVYREKSNVVGATFQGMCDANVAGGVVLPRTIS 303
Qy 303 LESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSPDFFAHFI 362
Db 304 LESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSPDFFAHFI 363
Qy 363 SKQSKQCLHNPRLDPFFKQAVCGNKLAGEBCDCGTEQDCALIGETCCDIATCRFKA 422
Db 364 SKQSKQCLHNPRLDPFFKQAVCGNKLAGEBCDCGTEQDCALIGETCCDIATCRFKA 423
Qy 423 GSNCAEGPCCNCLFMSKRCRPSFECDLPEYCNSSASCSPENHYVQTGHPCGLNQWI 482
Db 424 GSNCAEGPCCNCLFMSKRCRPSFECDLPEYCNSSASCSPENHYVQTGHPCGLNQWI 483
Qy 483 CIDGVCMSGDKQCTDTTFCGEVFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG 542
Db 484 CIDGVCMSGDKQCTDTTFCGEVFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCG 543
Qy 543 KLIKYYGKFLLOIPRATIIIVANISGHLCTIAVEFASDHADSQKWKIKDGTSCGSKNVCYRN 602
Db 544 KLIKYYGKFLLOIPRATIIIVANISGHLCTIAVEFASDHADSQKWKIKDGTSCGSKNVCYRN 603
Qy 603 QRCVSSVLYGDCYTDKNDRGVGNKHKCHCSASYLPPDCSVQSLWPGGSDSGNFPF 662
Db 604 QRCVSSVLYGDCYTDKNDRGVGNKHKCHCSASYLPPDCSVQSLWPGGSDSGNFPF 663
Qy 663 VAIIPARLPERRYENIYHSPMRPFLLFIPFFIFCVLIAMVKNVFORKKNRTEDYSS 722
Db 664 VAIIPARLPERRYENIYHSPMRPFLLFIPFFIFCVLIAMVKNVFORKKNRTEDYSS 723
Qy 723 DEQPESESEPKG 734
Db 724 DEQPESESEPKG 735

RESULT 2
Q6P2G0 ID Q6P2G0 PRELIMINARY; PRT; 579 AA.
AC AAH64547
AC AAH64547;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ADAM2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RL EMBL: BC064547; AAH64547.1; -.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR PRODOM; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00501; DISIN; 1.
DR PROSITE; PS02115; ADAM_MEPPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS02114; DISINTEGRIN_2; 1.
SQ SEQUENCE 579 AA; 64795 MW; 1F7AF0CDA2A064F9 CRC64;

Query Match 32.8%; Score 241; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.7e-233; Indels 0; Gaps 0;
Matches 241; Conservative 0; Mismatches 0;

Qy 297 HPTISLESIAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSPFE 356
Db 172 HPTISLESIAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKIFSNCSPFE 231
Qy 357 DFAHFTSKQSKQCLHNPRLDPFFKQAVCGNKLAGEBCDCGTEQDCALIGETCCDIA 416
Db 232 DFAHFTSKQSKQCLHNPRLDPFFKQAVCGNKLAGEBCDCGTEQDCALIGETCCDIA 291
Qy 417 TCRFKAGSNCAEGPCCNCLFMSKRCRPSFECDLPEYCNSSASCSPENHYVQTGHPC 476
Db 292 TCRFKAGSNCAEGPCCNCLFMSKRCRPSFECDLPEYCNSSASCSPENHYVQTGHPC 351
Qy 477 GLNQWICIDGVCMSGDKQCTDTTFCGEVFGPSECYSHLNSKTDVSGNCGISDSGYTQCEA 536
Db 352 GLNQWICIDGVCMSGDKQCTDTTFCGEVFGPSECYSHLNSKTDVSGNCGISDSGYTQCEA 411
Qy 537 D 537
Db 412 D 412

RESULT 3
AAH64547 ID AAH64547 PRELIMINARY; PRT; 579 AA.
AC AAH64547;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ADAM2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC064547; AA064547.1; -;
SQ SEQUENCE 579 AA; 64795 MW; 177AF0CDA2A064F9 CRC64;

Query Match 32.8%; Score 241; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.7e-233;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 297 HPTISLESIAVILIAQLLSMGITYDDINKKOCGAGVCIINPEAIHPSGKIFSNCSFE 356
Db 172 HPTISLESIAVILIAQLLSMGITYDDINKKOCGAGVCIINPEAIHPSGKIFSNCSFE 231
Qy 357 DFAHFISKQSKQLHNPRLDPPFPKQAVCNKLEAGEECDCGTEQDCALIGTCCDIA 416
Db 232 DFAHFISKQSKQLHNPRLDPPFPKQAVCNKLEAGEECDCGTEQDCALIGTCCDIA 291
Qy 417 TCRFKAGSNCAEGPCCNCLFMSKRCRPSFECSDLPEYCNCGSSASCPENHYVQTGHPC 476
Db 292 TCRFKAGSNCAEGPCCNCLFMSKRCRPSFECSDLPEYCNCGSSASCPENHYVQTGHPC 351
Qy 477 GLNQCICIDGVCMSGDKQCTDTFCGEVEFGSECVSHLNSKNTDVSNGCGISDSGYTQCEA 536
Db 352 GLNQCICIDGVCMSGDKQCTDTFCGEVEFGSECVSHLNSKNTDVSNGCGISDSGYTQCEA 411
Qy 537 D 537.
Db 412 D 412

RESULT 4
AD02 MACFA
ID AD02 MACFA STANDARD; PRT; 735 AA.
AC Q28478: Q28472;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
GN Name=ADAM2; Synonyms=FTNB;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95260313; PubMed=7741716;
RA Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
RT "Cloning and analysis of monkey fertilin reveals novel alpha subunit
RT isoforms";
RL Biochem. J. 307:843-850 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96341733; PubMed=8720115;
RA Ramarao C.S., Myles D.G., White J.M., Primakoff P.;
RT "Initial evaluation of fertilin as an immun contraceptive antigen and
RT molecular cloning of the cynomolgus monkey fertilin beta subunit.";
RL Mol. Reprod. Dev. 43:70-75 (1996).
CC -1- FUNCTION: Sperm surface membrane protein that may be involved in

CC sperm-egg plasma membrane adhesion and fusion during
CC fertilization. Could have a direct role in sperm-zona binding or
CC migration of sperm from the uterus into the oviduct. Interactions
CC with egg membrane could be mediated via binding between its
CC disintegrin-like domain to one or more integrins receptors on the
CC egg. This is a non catalytic metalloprotease-like protein (By
CC similarity).
CC -1- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -1- DOMAIN: A tripeptide motif (FDE) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding (By similarity).
CC -1- PTM: The signal and the metalloprotease domain are cleaved during
CC the epididymal maturation of the spermatozoa (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X77653; CAA54733.1; -;
CC EMBL: U33953; AB52699.1; -;
CC PIR: G02937; G02937.
CC HSP: P30403; IN4Y.
CC MEROPS: M12.950; -;
CC InterPro: IPR006586; ADAM cysteine.
CC InterPro: IPR001762; Disintegrin.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR006209; EGF_like.
CC InterPro: IPR001590; Peptidase_M12B.
CC Pfam: PF00200; Disintegrin; 1.
CC Pfam: PF01562; Pep M12B propep; 1.
CC Pfam: PF01421; Reptolysin; 1.
CC PRINTS: PR00289; Disintegrin.
CC ProDom: PD000664; Disintegrin; 1.
CC SMART: SM00608; ACR; 1.
CC SMART: SM00050; DISIN; 1.
CC PROSITE: PS0215; ADAM_MBP; 1.
CC PROSITE: PS00427; DISINTEGRIN_1; 1.
CC PROSITE: PS00244; DISINTEGRIN_2; 1.
CC PROSITE: PS00022; EGF_1; FALSE_NEG.
CC PROSITE: PS01186; EGF_2; FALSE_NEG.
CC PROSITE: PS00026; EGF_3; 1.
CC Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 16 Potential.
FT PROPEP 17 174 By similarity.
FT CHAIN 175 735 ADAM 2.
FT DOMAIN 17 686 Extracellular (Potential).
FT TRANSMEM 687 707 Potential.
FT DOMAIN 708 735 Cytoplasmic (Potential).
FT DOMAIN 175 382 Metalloprotease-like.
FT DOMAIN 383 475 Disintegrin-like.
FT DOMAIN 476 606 Cys-rich.
FT DOMAIN 612 645 EGF-like.
FT DISULFID 287 370 By similarity.
FT DISULFID 329 354 By similarity.
FT DISULFID 445 458 Potential.
FT DISULFID 616 627 By similarity.
FT DISULFID 621 633 By similarity.
FT DISULFID 635 644 By similarity.
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 459 459 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 566 566 N-linked (GlcNAc..) (Potential).
FT CONFLICT 723 723 S -> T (in Ref. 2).
SQ SEQUENCE 735 AA; 82357 MW; BE84BE115E1D0B53 CRC64;

Query Match 7.1%; Score 52; DB 1; Length 735;
Best Local Similarity 100.0%; Pred. No. 7.4e-43; Indels 0; Gaps 0;
Matches 52; Conservative 0; Mismatches 0;

QY 117 LQPNVSYGIEPLESSVGFEHVIYQVKHKADVSLYNEKDIESRDLSPFKLQS 168
|||||
DB 118 LQPNVSYGIEPLESSVGFEHVIYQVKHKADVSLYNEKDIESRDLSPFKLQS 169
|||||

RESULT 5

Q866A8 PRELIMINARY; PRT; 735 AA.
ID Q866A8
AC Q866A8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fertilin beta.
GN Name=FTNB;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22872989; PubMed=14510675;
RA Day A.E., Quilter C.R., Sargent C.A., Mileham A.J.;
RT "Chromosomal mapping, sequence and transcription analysis of the
RL porcine fertilin beta gene (ADAM2).";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;

RA Day A.; (2004), Department of Applied Sciences, Anglia Polytechnic
RL University, Cambridge, United Kingdom.
RL EMBL: AJ309003; CAC84225.2; --
DR HSSP: P18619; 1FVL.
DR MEROPS; M12.950; --.
DR GO; GO:0004222; F-metalloendopeptidase activity; IEA.
DR GO; GO:0003676; F-nucleic acid binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; Disintegrin.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS50026; EGF 3; 1.
SQ SEQUENCE 735 AA; 81804 MW; 16F5554690AEF4AB CRC64;

Query Match 2.7%; Score 20; DB 2; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SFNITILSSLELWIDENKI 236
|||||

Db 218 SFNITILSSLELWIDENKI 237

RESULT 6

AD02 RABIT
ID AD02_RABIT STANDARD; PRT; 751 AA.
AC Q28660;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
GN Name=ADAM2; Synonyms=FTNB;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97071141; PubMed=8914066;
RA Hardy C.M., Holland M.K.;
RT "Cloning and expression of recombinant rabbit fertilin.";
RL Mol. Reprod. Dev. 45:107-116(1996).
CC -I- FUNCTION: Sperm surface membrane protein that may be involved in
CC sperm-egg plasma membrane adhesion and fusion during
CC fertilization. Could have a direct role in sperm-zona binding or
CC migration of sperm from the uterus into the oviduct. Interactions
CC with egg membrane could be mediated via binding between its
CC disintegrin-like domain to one or more integrins receptors on the
CC egg. This is a non catalytic metalloprotease-like protein (By
CC similarity).
CC SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -I- DOMAIN: A tripeptide motif (VGE) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding (By similarity).
CC -I- FTM: The signal and the metalloprotease domain are cleaved during
CC the epididymal maturation of the spermatozoa (By similarity).
CC -I- SIMILARITY: Belongs to peptidase family M12B.
CC -I- SIMILARITY: Contains 1 disintegrin domain.
CC -I- SIMILARITY: Contains 1 EGF-like domain.

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CC or send an email to license@isb-sib.ch).

EMBL: U46070; AAA93321.1; --
DR HSSP; P30403; 1NAY.
DR MEROPS; M12.950; --.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.

DR PROSITE; PS50026; EGF_3; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 16 Potential.
 FT PROPEP 17 173 By similarity.
 FT CHAIN 17 751 ADAM 2.
 FT DOMAIN 17 702 Extracellular (Potential).
 FT TRANSMEM 703 723 Potential.
 FT DOMAIN 724 751 Cytoplasmic (Potential).
 FT DOMAIN 174 381 Metalloprotease-like.
 FT DOMAIN 382 474 Disintegrin-like.
 FT DOMAIN 475 606 Cys-rich.
 FT DOMAIN 612 645 EGF-like.
 FT DISULFID 286 369 By similarity.
 FT DISULFID 328 353 By similarity.
 FT DISULFID 444 457 Potential.
 FT DISULFID 616 627 By similarity.
 FT DISULFID 621 633 By similarity.
 FT DISULFID 635 644 By similarity.
 FT CARBOHYD 122 147 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 219 219 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 352 352 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 559 559 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 566 566 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 643 643 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 751 AA; 83616 MW; 8246FBFC4A9FCE1 CRC64;

Query Match 2.7%; Score 20; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SFNITILSSLEWIDENKI 236
 |||||
 Db 217 SFNITILSSLEWIDENKI 236

RESULT 7
 AD02_CAVPO STANDARD; PRT; 735 AA.
 AC Q60411;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 03-JUN-2004 (Rel. 44, Last annotation update)
 DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
 GN (Fertilin beta subunit) (PH-30) (PH30).
 GN Name=ADAM2; Synonyms=FTNB;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94068486; PubMed=8248170;
 RA Wolfberg T.G., Bazan J.F., Blobel C.P., Myles D.G., Primakoff P.,
 RA White J.M.;
 RA "The precursor region of a protein active in sperm-egg fusion contains
 RT a metalloprotease and a disintegrin domain: structural, functional,
 RT and evolutionary implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10783-10787(1993).
 RN [2]
 RP SEQUENCE OF 383-735 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=92204234; PubMed=1552944;
 RA Blobel C.P., Wolfberg T.G., Turck C.W., Myles D.G., Primakoff P.,
 RA White J.M.;
 RA "A potential fusion peptide and an integrin ligand domain in a protein
 RT active in sperm-egg fusion.";
 RL Nature 356:248-252(1992).
 CC -1- FUNCTION: Sperm surface membrane protein that may be involved in

CC sperm-egg plasma membrane adhesion and fusion during
 CC fertilization. Could have a direct role in sperm-zona binding or
 CC migration of sperm from the uterus into the oviduct. Interactions
 CC with egg membrane could be mediated via binding between its
 CC disintegrin-like domain to one or more integrins receptors on the
 CC egg. This is a non catalytic metalloprotease-like protein (By
 CC similarity).
 CC -1- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed specifically in testis.
 CC -1- DEVELOPMENTAL STAGE: Expression begins during meiotic prophase.
 CC -1- DOMAIN: A tripeptide motif (TDE) within disintegrin-like domain
 CC could be involved in the binding to egg integrin receptor and thus
 CC could mediate sperm/egg binding (By similarity).
 CC -1- PTM: The signal and the metalloprotease domain are cleaved during
 CC the epididymal maturation of the spermatozoa (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -----
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 CC -----
 CC EMBL; Z11720; CAAT7784.1; -.
 DR HSSP; P18619; 1FVL.
 DR MEROPS; M12.950; -.
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001590; Peptidase M12B.
 DR InterPro; IPR002870; Peptidase M12B_N.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS50215; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS50026; EGF_3; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 15 Potential.
 FT PROPEP 16 176 By similarity.
 FT CHAIN 177 735 ADAM 2.
 FT DOMAIN 16 680 Extracellular (Potential).
 FT TRANSMEM 681 701 Potential.
 FT DOMAIN 702 735 Cytoplasmic (Potential).
 FT DOMAIN 178 382 Metalloprotease-like.
 FT DOMAIN 383 472 Disintegrin-like.
 FT DOMAIN 473 609 Cys-rich.
 FT DOMAIN 610 643 EGF-like.
 FT DISULFID 287 370 By similarity.
 FT DISULFID 329 354 By similarity.
 FT DISULFID 442 455 Potential.
 FT DISULFID 614 625 By similarity.
 FT DISULFID 619 631 By similarity.
 FT DISULFID 633 642 By similarity.
 SQ SEQUENCE 735 AA; 81904 MW; 7535FC39F44FB645 CRC64;

Query Match 2.5%; Score 18; DB 1; Length 735;
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 SYLVLRPHDVAFLVYRE 272
 |||||
 Db 256 SYLVLRPHDVAFLVYRE 273

RESULT 8
 AD18_MACFA STANDARD; PRT; 746 AA.
 AC Q95154;
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 01-OCT-2004 (Rel. 45, last annotation update)
 DE ADAM 18 precursor (A disintegrin and metalloproteinase domain 18)
 DE (Transmembrane metalloproteinase-like, disintegrin-like, and cysteine-rich protein III) (tmcd III).
 GN Name=ADAM18; Synonyms=TMDC3;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98328566; PubMed=9665629;
 RA Frayne J., Jury J.A., Barker H.L., Perry A.C.F., Jones R., Hall L.;
 RT "Macaque MDC family of proteins: sequence analysis, tissue distribution and processing in the male reproductive tract";
 RL Mol. Hum. Reprod. 4:429-437(1998).
 CC -1- FUNCTION: Sperm surface membrane protein that may be involved in spermatogenesis and fertilization. This is a non catalytic metalloproteinase-like protein (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in adult and prepubertal testis.
 CC -1- DOMAIN: A tripeptide motif (ECD) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding (By similarity).
 CC -1- PTM: The prodomain and the metalloproteinase-like domain are cleaved during the epididymal maturation of the spermatozoa.
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
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 CC EMBL; Y08617; CAA69909.1; -;
 CC HSSP; P83469; IMPZ.
 CC MEROPS: M12.957; -;
 CC InterPro; IPR006586; ADAM cysteine.
 CC InterPro; IPR001762; Disintegrin.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR001590; Peptidase M12B.
 CC InterPro; IPR002870; Peptidase_M12B_N.
 CC Pfam; PF00200; Disintegrin; 1.
 CC Pfam; PF01562; Pep M12B_propep; 1.
 CC Pfam; PF01421; Reprolysin; 1.
 CC ProDom; PD000664; Disintegrin; 1.
 CC SMART; SM00608; ACR; 1.
 CC SMART; SM00050; DISIN; 1.
 CC PROSITE; PS00215; ADAM_MERPRO; 1.
 CC PROSITE; PS00427; DISINTEGRIN 1; FALSE_NEG.
 CC PROSITE; PS00214; DISINTEGRIN 2; 1.
 CC PROSITE; PS00022; EGF_1; FALSE_NEG.

DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 KW PROSITE; PS00026; EGF_3; 1.
 KW EGF-like domain; Glycoprotein; Signal; Spermatogenesis; Transmembrane.
 FT SIGNAL 1 16 Potential.
 FT PROPEP 17 183 Potential.
 FT CHAIN 184 746 ADAM 18.
 FT DOMAIN 177 687 Extracellular (Potential).
 FT TRANSMEM 688 708 Potential.
 FT DOMAIN 709 746 Cytoplasmic (Potential).
 FT DOMAIN 184 389 Metalloproteinase-like.
 FT DOMAIN 390 479 Disintegrin-like.
 FT DOMAIN 480 619 Cys-rich.
 FT DOMAIN 620 654 EGF-like.
 FT DISULFID 293 376 By similarity.
 FT DISULFID 335 360 By similarity.
 FT DISULFID 458 483 Potential.
 FT DISULFID 624 636 By similarity.
 FT DISULFID 630 642 By similarity.
 FT DISULFID 644 653 By similarity.
 FT CARBOHYD 36 36 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 122 122 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 149 149 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 156 156 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 177 177 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 294 294 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 359 359 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 465 465 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 611 611 N-linked (GLNAC. .) (Potential).
 FT CARBOHYD 625 625 N-linked (GLNAC. .) (Potential).
 SQ SEQUENCE 746 AA; 84448 MW; 1D8C7E9071502E30 CRC64;
 Query Match 2.2%; Score 16; DB 1; Length 746;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 LQFENVSYGIEPLESS 132
 |||||
 Db 118 LQFENVSYGIEPLESS 133

RESULT 9
 Q6ZWLI PRELIMINARY; PRT; 279 AA.
 ID Q6ZWLI;
 AC Q6ZWLI;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 03-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ16017.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
 RA Kaeriyama Y., Moriya S., Chiba E., Momiya H., Onogawa S.,
 RA Raga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
 RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
 RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Yamashita H., Mateuo K., Nakamura Y., Sekine M.,
 RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
 RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK122608; BAC85489.1; -;
 DR InterPro; IPR001590; Peptidase M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR Pfam; PF01562; Pep M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR PROSITE; PS00215; ADAM_MERPRO; 1.


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Query Match      2.0%; Score 15; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR PROSITE; PS50214; DISINTEGRIN 2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS0026; EGF_3; 1.
KW INTEGRIN; Metalloprotease; Protease.
SQ SEQUENCE 787 AA; 87931 MW; CE0F54A50466B336 CRC64;

Query Match      2.0%; Score 15; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPLES 131
DB 121 LQFENVSYGIEPLES 135

RESULT 12
Q8TC42 PRELIMINARY; PRT; 787 AA.
AC Q8TC42;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A disintegrin and metalloprotease domain 32.
GN Name=ADAM32;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Worley K.C., Hate S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallay D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026085; AAH26085.1; -.
DR HSSP; P30403; IN4Y.
DR MEROPS; M12.960; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
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RC TISSUE=Testis;
 RX MEDLINE=97304362; PubMed=9160725;
 RA Waters S.I., White J.M.;
 RT "Biochemical and molecular characterization of bovine fertilin alpha
 and beta (ADAM 1 and ADAM 2): a candidate sperm-egg binding/fusion
 complex";
 RL Biol. Reprod. 56:1245-1254(1997).
 CC -!- FUNCTION: Sperm surface membrane protein that may be involved in
 sperm-egg plasma membrane adhesion and fusion during
 fertilization. Could have a direct role in sperm-zona binding or
 migration of sperm from the uterus into the oviduct. Interactions
 with egg membrane could be mediated via binding between its
 disintegrin-like domain to one or more integrins receptors on the
 egg. This is a non catalytic metalloprotease-like protein (By
 similarity).
 CC -!- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed specifically in testis.
 CC -!- DOMAIN: A tripeptide motif (TDE) within disintegrin-like domain
 could be involved in the binding to egg integrin receptor and thus
 could mediate sperm/egg binding (By similarity).
 CC -!- PTM: The signal and the metalloprotease domain are cleaved during
 the epididymal maturation of the spermatozoa (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M12B.
 CC -!- SIMILARITY: Contains 1 disintegrin domain.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF086808; AAC62753.1; -
 DR HSSP; P18619; 1FVL.
 DR MEROPS; M12.950; -
 DR InterPro; IPR006586; ADAM_cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR008994; Nucleic acid OB.
 DR InterPro; IPR001590; Peptidase M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR Pfam; PF00200; Disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysein; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS50215; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS50026; EGF_3; 1.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 16
 FT PROPEP 17 174 Potential.
 FT CHAIN 175 745 By similarity.
 FT DOMAIN 17 696 ADAM 2.
 FT TRANSHEM 697 717 Extracellular (Potential).
 FT DOMAIN 718 745 Potential.
 FT DOMAIN 175 382 Cytoplasmic (Potential).
 FT DOMAIN 383 474 Metalloprotease-like.
 FT DOMAIN 475 605 Disintegrin-like.
 FT DOMAIN 606 644 Cys-rich.
 FT DOMAIN 611 644 EGF-like.
 FT DOMAIN 148 151 Poly-Ser.
 FT DISULFID 287 370 By similarity.

FT DISULFID 329 354 By similarity.
 FT DISULFID 444 457 Potential.
 FT DISULFID 615 626 By similarity.
 FT DISULFID 620 632 By similarity.
 FT DISULFID 634 643 By similarity.
 FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 558 558 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 745 AA; 83150 MW; B5D9DC0168999B00 CRC64;
 Query Match 1.9%; Score 14; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 LOFENVSYGIEPLE 130
 Db 118 LOFENVSYGIEPLE 131
 RESULT 15
 Q8BJ80 PRELIMINARY; PRT; 677 AA.
 ID Q8BJ80 AC Q8BJ80; DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:1700008E04 product:METALLOPROTEASE/DISINTEGRIN
 DE homolog.
 GN Name=Adam32;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium,
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakauchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT WIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.,
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005759; BAC25124.1; -.
DR HSSP; P18619; 1FVL.
DR MGD; MGI:2653822; Adam32.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KW Integrin; Metalloprotease; Protease.
SQ SEQUENCE 677 AA; 75934 MW; 985CD38F26EDCF9F CRC64;

Query Match 1.8%; Score 13; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LQFENVSYGIEPL 129
| | | | | | | | | |
Db 122 LQFENVSYGIEPL 134

Search completed: January 10, 2005, 22:38:07
Job time : 204 secs

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OM protein - protein search, using sw model

Run on: January 10, 2005, 22:09:32 ; Search time 40 Seconds
(without alignments)
1216.935 Million cell updates/sec

Title: US-10-054-683-19

Perfect score: 3984

Sequence: 1 MWVFLSLGLGRLMDSNFD.....WRTDYSSDQPESEBPKG 734

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3984	100.0	734	2	US-08-765-243-8
2	3984	100.0	734	5	PCT-US95-07295-8
3	3551	89.1	651	1	US-08-284-101-2
4	3551	89.1	651	2	US-08-765-243-2
5	3551	89.1	651	5	PCT-US95-07295-2
6	2440	61.2	735	2	US-08-765-243-6
7	2440	61.2	735	5	PCT-US95-07295-6
8	1512	38.0	457	1	US-08-284-101-4
9	1512	38.0	457	2	US-08-765-243-4
10	1512	38.0	457	5	PCT-US95-07295-4
11	1506.5	37.8	787	4	US-10-000-489-70
12	1493.5	37.5	715	4	US-10-140-002-116
13	948.5	23.8	790	4	US-10-140-002-204
14	937	23.5	722	4	US-09-617-145-2
15	843.5	21.2	775	4	US-09-786-256C-15
16	843.5	21.2	775	4	US-09-786-256C-32
17	764	19.2	812	4	US-09-632-098-4
18	764	19.2	812	4	US-10-177-308-4
19	764	19.2	849	4	US-09-548-797B-6
20	752.5	18.9	606	4	US-09-460-295B-12
21	739	18.5	832	4	US-09-634-252A-4
22	723	18.1	613	4	US-09-026-001A-10
23	721.5	18.1	696	3	US-09-351-414-2
24	721	18.1	814	3	US-09-813-819-4
25	721	18.1	814	3	US-09-920-048-4
26	720	18.1	821	4	US-09-026-001A-18
27	720	18.1	855	3	US-09-813-819-2

28	720	18.1	855	3	US-09-920-048-2	Sequence 2, Appli
29	718	18.0	787	4	US-09-548-797B-5	Sequence 5, Appli
30	717	18.0	621	4	US-09-026-001A-6	Sequence 6, Appli
31	714.5	17.9	571	4	US-09-460-295B-13	Sequence 13, Appli
32	709.5	17.8	616	4	US-09-608-790-1	Sequence 1, Appli
33	701	17.6	802	4	US-09-632-098-2	Sequence 2, Appli
34	701	17.6	802	4	US-10-177-308-2	Sequence 2, Appli
35	700	17.6	769	1	US-08-243-542-4	Sequence 4, Appli
36	700	17.6	769	1	US-08-477-407-4	Sequence 4, Appli
37	700	17.6	769	1	US-08-484-355-4	Sequence 4, Appli
38	698	17.5	670	1	US-08-243-542-3	Sequence 3, Appli
39	698	17.5	670	1	US-08-477-407-3	Sequence 3, Appli
40	698	17.5	670	1	US-08-484-355-3	Sequence 3, Appli
41	698	17.5	867	4	US-09-634-252A-6	Sequence 6, Appli
42	692	17.4	751	2	US-08-836-443-3	Sequence 3, Appli
43	679.5	17.1	592	4	US-09-026-001A-14	Sequence 14, Appli
44	667.5	16.8	746	4	US-09-548-797B-4	Sequence 4, Appli
45	665.5	16.7	540	4	US-09-786-256C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-765-243-8
; Sequence 8, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 125 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-243-8

Query Match	100.0%;	Score 3984;	DB 2;	Length 734;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 734;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MWVFLSLGLGRLMDSNFDSPVQITVPKIRSIKEGIESQASYKIVIEGKPYTNLM	60	
Db	1	MWVFLSLGLGRLMDSNFDSPVQITVPKIRSIKEGIESQASYKIVIEGKPYTNLM	60	
QY	61	QKNFLPHNFRVYSYSGTGMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGLQFE	120	

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Db      61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLQFE 120
QY      121 NVSYGIEPLESSVGFVHVIYQVHKKADVSLYNEKDIESRDLSPKLSAEPQDPFAKYLE 180
Db      121 NVSYGIEPLESSVGFVHVIYQVHKKADVSLYNEKDIESRDLSPKLSAEPQDPFAKYLE 180
QY      181 MHVIVEKQLYNHMGSDTTVAQKVFQGLITNAIFVSNITIISSLELWIDENKIATTG 240
Db      181 MHVIVEKQLYNHMGSDTTVAQKVFQGLITNAIFVSNITIISSLELWIDENKIATTG 240
QY      241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDAANYAGGVVLHPRT 300
Db      241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDAANYAGGVVLHPRT 300
QY      301 ISLESIAVILAQLLSLNGITDYDDINKQCCGAVCINMPEAIHFSGVKIPFNSCSFEDFAH 360
Db      301 ISLESIAVILAQLLSLNGITDYDDINKQCCGAVCINMPEAIHFSGVKIPFNSCSFEDFAH 360
QY      361 FISKQSOCLHNPRLDPPFKQAVCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRF 420
Db      361 FISKQSOCLHNPRLDPPFKQAVCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRF 420
QY      421 KAGSNCAEGPCCECLFMSKERMCRPSFECDLPEYCNSSASCPENHYVQTGHPCGLNQ 480
Db      421 KAGSNCAEGPCCECLFMSKERMCRPSFECDLPEYCNSSASCPENHYVQTGHPCGLNQ 480
QY      481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db      481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
QY      541 CGKLI CKYVGFLLQIPRATIIYANISGHLCTAIEFASDHADSOXMIKDTSCGSKNVC 600
Db      541 CGKLI CKYVGFLLQIPRATIIYANISGHLCTAIEFASDHADSOXMIKDTSCGSKNVC 600
QY      601 RNQRCVSSSYLVGYDCTTDCNDRGVNKNKCHCSASYLPDPCSVQSDLPFGGSIDSGNF 660
Db      601 RNQRCVSSSYLVGYDCTTDCNDRGVNKNKCHCSASYLPDPCSVQSDLPFGGSIDSGNF 660
QY      661 PPVAIPARLPERRYIENIYHSPKMRWPFLLPFFIIFCVLIATMVKVNFQKRWRTEDY 720
Db      661 PPVAIPARLPERRYIENIYHSPKMRWPFLLPFFIIFCVLIATMVKVNFQKRWRTEDY 720
QY      721 SSDEQPESESEPKG 734
Db      721 SSDEQPESESEPKG 734

```

RESULT 2

PCT-US95-07295-8

Sequence 8, Application PC/TUS9507295

GENERAL INFORMATION:

APPLICANT: ALVES, KENNETH

APPLICANT: GUPTA, SUNIL K.

APPLICANT: HOLLIS, GREGORY F.

TITLE OF INVENTION: CONTRACEPTIVE VACCINE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: MARY A. APOLLINA

STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

CITY: RAYWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07295

FILING DATE:

CLASSIFICATION:

RESULT 3

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; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07295-8

```

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Query Match      100.0%; Score 3984; DB 5; Length 734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MWVFLLSGLGGLRMDNSFDSLPVQITVPEKIRSIIEGIESQASYKIVIEGKPYTVNLM 60
Db      1 MWVFLLSGLGGLRMDNSFDSLPVQITVPEKIRSIIEGIESQASYKIVIEGKPYTVNLM 60
QY      61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLQFE 120
Db      61 QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQYIEGYPKSVVMVSTCTGLRGVLQFE 120
QY      121 NVSYGIEPLESSVGFVHVIYQVHKKADVSLYNEKDIESRDLSPKLSAEPQDPFAKYLE 180
Db      121 NVSYGIEPLESSVGFVHVIYQVHKKADVSLYNEKDIESRDLSPKLSAEPQDPFAKYLE 180
QY      181 MHVIVEKQLYNHMGSDTTVAQKVFQGLITNAIFVSNITIISSLELWIDENKIATTG 240
Db      181 MHVIVEKQLYNHMGSDTTVAQKVFQGLITNAIFVSNITIISSLELWIDENKIATTG 240
QY      241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDAANYAGGVVLHPRT 300
Db      241 EANELLHTFLRWKTSYLVLRPHDVAFLVYREKSNYVGATFGQKMCDAANYAGGVVLHPRT 300
QY      301 ISLESIAVILAQLLSLNGITDYDDINKQCCGAVCINMPEAIHFSGVKIPFNSCSFEDFAH 360
Db      301 ISLESIAVILAQLLSLNGITDYDDINKQCCGAVCINMPEAIHFSGVKIPFNSCSFEDFAH 360
QY      361 FISKQSOCLHNPRLDPPFKQAVCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRF 420
Db      361 FISKQSOCLHNPRLDPPFKQAVCGNAKLEAGEBCDCGTEQDCALIGETCCDIATCRF 420
QY      421 KAGSNCAEGPCCECLFMSKERMCRPSFECDLPEYCNSSASCPENHYVQTGHPCGLNQ 480
Db      421 KAGSNCAEGPCCECLFMSKERMCRPSFECDLPEYCNSSASCPENHYVQTGHPCGLNQ 480
QY      481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
Db      481 WICIDGVCMSGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQ 540
QY      541 CGKLI CKYVGFLLQIPRATIIYANISGHLCTAIEFASDHADSOXMIKDTSCGSKNVC 600
Db      541 CGKLI CKYVGFLLQIPRATIIYANISGHLCTAIEFASDHADSOXMIKDTSCGSKNVC 600
QY      601 RNQRCVSSSYLVGYDCTTDCNDRGVNKNKCHCSASYLPDPCSVQSDLPFGGSIDSGNF 660
Db      601 RNQRCVSSSYLVGYDCTTDCNDRGVNKNKCHCSASYLPDPCSVQSDLPFGGSIDSGNF 660
QY      661 PPVAIPARLPERRYIENIYHSPKMRWPFLLPFFIIFCVLIATMVKVNFQKRWRTEDY 720
Db      661 PPVAIPARLPERRYIENIYHSPKMRWPFLLPFFIIFCVLIATMVKVNFQKRWRTEDY 720
QY      721 SSDEQPESESEPKG 734
Db      721 SSDEQPESESEPKG 734

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US-08-264-101-2
; Sequence 2, Application US/08264101
; Patent No. 5693496
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,101
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-264-101-2

Query Match      89.1%; Score 3551; DB 1; Length 651;
Best Local Similarity 100.0%; Pred. No. 4.3e-284;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      85 QDFQNFCHYQGYEGYKPKSVVMYSTCTGLRGVLQFENVSYGIEPLLESSVGFHVIYQVKH 144
Db      2 QDFQNFCHYQGYEGYKPKSVVMYSTCTGLRGVLQFENVSYGIEPLLESSVGFHVIYQVKH 61

Qy      145 KKADVSLYNEKDIESRDLSPKLSAEPQDQFQAKYIEMHVIKQLYNHMGSDTTTVAQKV 204
Db      62 KKADVSLYNEKDIESRDLSPKLSAEPQDQFQAKYIEMHVIKQLYNHMGSDTTTVAQKV 121

Qy      205 FQILGLTNALFVSNFTIILSSLELWIDENKIATTTGEANELLHTFLRWKTSYLVLRPHDV 264
Db      122 FQILGLTNALFVSNFTIILSSLELWIDENKIATTTGEANELLHTFLRWKTSYLVLRPHDV 181

Qy      265 AFLVVRKSNYYGATFQGMKCDANVAGGVVLPRTISLESIAVILAQLLSLNGITYDD 324
Db      182 AFLVVRKSNYYGATFQGMKCDANVAGGVVLPRTISLESIAVILAQLLSLNGITYDD 241

Qy      325 INKQCQSGAVICINPEAIHFSGVKIFSNCSFEDFAHFIKSKQSOCLHNQRLDPFFKQQA 384
Db      242 INKQCQSGAVICINPEAIHFSGVKIFSNCSFEDFAHFIKSKQSOCLHNQRLDPFFKQQA 301

Qy      385 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGNCNCAEGPCCNCLFMSKERM 444
Db      302 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGNCNCAEGPCCNCLFMSKERM 361

Qy      445 RPSFECDLPEYCNCGSSASCPENHYQTGHPGCLNOMICIDGCMGSDKQCTDTFGKEVE 504
Db      362 RPSFECDLPEYCNCGSSASCPENHYQTGHPGCLNOMICIDGCMGSDKQCTDTFGKEVE 421
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US-08-765-243-2
; Sequence 2, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-243-2

Query Match      89.1%; Score 3551; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 4.3e-284;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      85 QDFQNFCHYQGYEGYKPKSVVMYSTCTGLRGVLQFENVSYGIEPLLESSVGFHVIYQVKH 144
Db      2 QDFQNFCHYQGYEGYKPKSVVMYSTCTGLRGVLQFENVSYGIEPLLESSVGFHVIYQVKH 61

Qy      145 KKADVSLYNEKDIESRDLSPKLSAEPQDQFQAKYIEMHVIKQLYNHMGSDTTTVAQKV 204
Db      62 KKADVSLYNEKDIESRDLSPKLSAEPQDQFQAKYIEMHVIKQLYNHMGSDTTTVAQKV 121

Qy      205 FQILGLTNALFVSNFTIILSSLELWIDENKIATTTGEANELLHTFLRWKTSYLVLRPHDV 264
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Db 122 FQILGLTNAIFVSNITILSLELWIDENKIATTCGEANELLHTFLRWKTSYLVLRPHDV 181
Qy 265 AFLVYREKSNVYGATFGKMCNDANYAGVVLHPTTISLESILAVILAQLLSLMSGITYDD 324
Db 182 AFLVYREKSNVYGATFGKMCNDANYAGVVLHPTTISLESILAVILAQLLSLMSGITYDD 241
Qy 325 INKQCQSGAVCIMNPEAIFHSGVKIFSNCSFEDFAHFIKQSKQCLHNQRLDPFFKQQA 384
Db 242 INKQCQSGAVCIMNPEAIFHSGVKIFSNCSFEDFAHFIKQSKQCLHNQRLDPFFKQQA 301
Qy 385 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 444
Db 302 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 361
Qy 445 RPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQWICIDGVCMGSDKQCTDTFGKEVE 504
Db 362 RPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQWICIDGVCMGSDKQCTDTFGKEVE 421
Qy 505 FGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLI CKYVGFLLQIPRATIYA 564
Db 422 FGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLI CKYVGFLLQIPRATIYA 481
Qy 565 NISGHLCIAVEFASDHADSQKWKIDGTS CGSNKVCNRQCVSSSYLGVDCTTDKCDNRG 624
Db 482 NISGHLCIAVEFASDHADSQKWKIDGTS CGSNKVCNRQCVSSSYLGVDCTTDKCDNRG 541
Qy 625 VCNNKXKHCASLYLPDCSVQSDLPFGGSDSGNFPFPPVAIPARLPERRRYENIYHSPKM 684
Db 542 VCNNKXKHCASLYLPDCSVQSDLPFGGSDSGNFPFPPVAIPARLPERRRYENIYHSPKM 601
Qy 685 RWPFFLPIFPFIIFCVLIAIMVKNVFNQKWKRTEDYSSDEQPESEPKG 734
Db 602 RWPFFLPIFPFIIFCVLIAIMVKNVFNQKWKRTEDYSSDEQPESEPKG 651

RESULT 5

PCT-US95-07295-2
; Sequence 2, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
PCT-US95-07295-2

Query Match 89.1%; Score 3551; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 4.3e-284; Indels 0; Gaps 0;
Matches 650; Conservative 0; Mismatches 0;

Qy 85 QDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFHEVIYQVXH 144
Db 2 QDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFHEVIYQVXH 61
Qy 145 KKADVSLYNEKDIIESRDLSPKLOSABPQDFAKYIEMHVIIVEKQLYNHMGSDTTVVAQKV 204
Db 62 KKADVSLYNEKDIIESRDLSPKLOSABPQDFAKYIEMHVIIVEKQLYNHMGSDTTVVAQKV 121
Qy 205 FQILGLTNAIFVSNITILSLELWIDENKIATTCGEANELLHTFLRWKTSYLVLRPHDV 264
Db 122 FQILGLTNAIFVSNITILSLELWIDENKIATTCGEANELLHTFLRWKTSYLVLRPHDV 181
Qy 265 AFLVYREKSNVYGATFGKMCNDANYAGVVLHPTTISLESILAVILAQLLSLMSGITYDD 324
Db 182 AFLVYREKSNVYGATFGKMCNDANYAGVVLHPTTISLESILAVILAQLLSLMSGITYDD 241
Qy 325 INKQCQSGAVCIMNPEAIFHSGVKIFSNCSFEDFAHFIKQSKQCLHNQRLDPFFKQQA 384
Db 242 INKQCQSGAVCIMNPEAIFHSGVKIFSNCSFEDFAHFIKQSKQCLHNQRLDPFFKQQA 301
Qy 385 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 444
Db 302 VCGNAKLEAGEECDCGTEQDCALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERM 361
Qy 445 RPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQWICIDGVCMGSDKQCTDTFGKEVE 504
Db 362 RPSFECDLPEYCNCGSSASCPENHYVQTGHPCGLNQWICIDGVCMGSDKQCTDTFGKEVE 421
Qy 505 FGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLI CKYVGFLLQIPRATIYA 564
Db 422 FGPSECVSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLI CKYVGFLLQIPRATIYA 481
Qy 565 NISGHLCIAVEFASDHADSQKWKIDGTS CGSNKVCNRQCVSSSYLGVDCTTDKCDNRG 624
Db 482 NISGHLCIAVEFASDHADSQKWKIDGTS CGSNKVCNRQCVSSSYLGVDCTTDKCDNRG 541
Qy 625 VCNNKXKHCASLYLPDCSVQSDLPFGGSDSGNFPFPPVAIPARLPERRRYENIYHSPKM 684
Db 542 VCNNKXKHCASLYLPDCSVQSDLPFGGSDSGNFPFPPVAIPARLPERRRYENIYHSPKM 601
Qy 685 RWPFFLPIFPFIIFCVLIAIMVKNVFNQKWKRTEDYSSDEQPESEPKG 734
Db 602 RWPFFLPIFPFIIFCVLIAIMVKNVFNQKWKRTEDYSSDEQPESEPKG 651

RESULT 6

US-08-765-243-6
; Sequence 6, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-765-243-6

Query Match 61.2%; Score 2440; DB 2; Length 735;
Best Local Similarity 59.6%; Pred. No. 1.9e-192;
Matches 439; Conservative 119; Mismatches 167; Indels 12; Gaps 7;

QY 3 VFLLSG---LGL---RMDSNFDSLVPQITVPEKIRSIIEGIESQASYKIVIEGKPYT 56
DB 4 ILLLSGLSELGSLQSQTETREKLVHVQVTPPEKIRSVTSNGVETQVTYNLKEGKTYT 63

QY 57 VNLMOKNFLPHNFRVSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGV 116
DB 64 LDLMQKPFLLPNFRVSYDNAGIMRSLEQRFQNICYFQGYIEGYPNSWIVSTCTGLRGF 123

QY 117 LQFENVSYGIEPLESSVGFPHVYQVKKADVSLYNEKDIESRDLSEFKLSAEPQDFA 176
DB 124 LQFENVSYGIEPLESSVGFPHVYQVPEKGGALLAEKIDILRDSQYKIRSIKQPIVS 183

QY 177 KYTEMHVIKQLYNHMGSDTTVAQKVFOLIGLTNAIFVSNITILSSLEWIDENKI 236
DB 184 HYLEIHIVKQMFHEIGADTAIVTQKIFOLIGLANAIFAPFNLTVILSSLEFWMENKI 243

QY 237 ATTGEANELHTLRLWKTSLVLRPHDVAFLVYREKSNVYGVATFOGKMDANYAGGVVL 296
DB 244 LTTGDANKLYRFLKWKQSYLVRPHDMAFLVYRNTTVDYGVATYQGMCDKNYAGGVAL 303

QY 297 HPRTISLESIAVLAQLLSMGIYDDINKCQCSGAVCIMNPEAIFHSGVKIFSNCSFE 356
DB 304 HPKAVTLESIAIILVQLLSMGLAYDDVNNKCCQGVPCVMNPEAPHSSGVRAFSNCSME 363

QY 357 DPAHFISKQSKQLHNQPRLDPPFKQAVCGNAKLEAGEBCDCGTQDCCALIGETCCDIA 416
DB 364 DFKFITTSQSSHLQONQPTLQPSYK-MAVCGNGEVEDEICDGG-KKGCAMPPPCNPD 421

QY 417 TCRFKAGSNCAEGPCENCLFMSKERMCPSFECDLPYCNSSASCENPHVYVOTGHPC 476
DB 422 TKLSDSGSCSGICNSCKLKRGEVCRUAQDECDVTEYCNSTSEVC-EDDFVQNGHPC 480

QY 477 GLNQWICIDGVMGSKQKQCTDTFGKEVGFSPSEYCSYHLSKTDVSGNCGISDSGYTQCEA 536
DB 481 DNRKWCINGTCQSGEQCDLFGIDAGFSSSECFWELNSKSDISGSCGISAGYKECPP 540

QY 537 DNLQCKGLICKYGVKFLQIIPRATIIYANISGHLCIAVEFASDHADSKQWIKDGTSCGS 596
DB 541 NDRMCKGIIICKYQSENILKRSATVIYANISGHVCSLEYPOGHNESQKMWVRDGTVCGS 600

QY 597 NKVCRNORCVSSYLVGDCITTDKNDRGVNNKHKHCHCSASYLPPDCSVQSLWPQGSID 656
DB 601 NKVQONQKQVADTFLGVDNLEKNHGVNNKKNCHCDPTLPPDCRKNKDSYPGGSID 660

QY 657 SGNFPPVAIPARLPERRIENIYHSPMRPFLLFPFFIIFCVLIAMVKNVFORKKWR 716
DB 661 SGN-KERAEP--IPVRPIASRYRSKSPRPFLLIIPFFVIVLVLGMLVKVYSQRKKWR 717

QY 717 TEDIYSDDEQESSEPK 733
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```
DB 718 MDDFSSEQFESESESK 734

RESULT 7
PCT-US95-07295-6
; Sequence 6, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07295-6

Query Match 61.2%; Score 2440; DB 5; Length 735;
Best Local Similarity 59.6%; Pred. No. 1.9e-192;
Matches 439; Conservative 119; Mismatches 167; Indels 12; Gaps 7;

QY 3 VFLLSG---LGL---RMDSNFDSLVPQITVPEKIRSIIEGIESQASYKIVIEGKPYT 56
DB 4 ILLLSGLSELGSLQSQTETREKLVHVQVTPPEKIRSVTSNGVETQVTYNLKEGKTYT 63

QY 57 VNLMOKNFLPHNFRVSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGV 116
DB 64 LDLMQKPFLLPNFRVSYDNAGIMRSLEQRFQNICYFQGYIEGYPNSWIVSTCTGLRGF 123

QY 117 LQFENVSYGIEPLESSVGFPHVYQVKKADVSLYNEKDIESRDLSEFKLSAEPQDFA 176
DB 124 LQFENVSYGIEPLESSVGFPHVYQVPEKGGALLAEKIDILRDSQYKIRSIKQPIVS 183

QY 177 KYTEMHVIKQLYNHMGSDTTVAQKVFOLIGLTNAIFVSNITILSSLEWIDENKI 236
DB 184 HYLEIHIVKQMFHEIGADTAIVTQKIFOLIGLANAIFAPFNLTVILSSLEFWMENKI 243

QY 237 ATTGEANELHTLRLWKTSLVLRPHDVAFLVYREKSNVYGVATFOGKMDANYAGGVVL 296
DB 244 LTTGDANKLYRFLKWKQSYLVRPHDMAFLVYRNTTVDYGVATYQGMCDKNYAGGVAL 303

QY 297 HPRTISLESIAVLAQLLSMGIYDDINKCQCSGAVCIMNPEAIFHSGVKIFSNCSFE 356
DB 304 HPKAVTLESIAIILVQLLSMGLAYDDVNNKCCQGVPCVMNPEAPHSSGVRAFSNCSME 363

QY 357 DPAHFISKQSKQLHNQPRLDPPFKQAVCGNAKLEAGEBCDCGTQDCCALIGETCCDIA 416
DB 364 DFKFITTSQSSHLQONQPTLQPSYK-MAVCGNGEVEDEICDGG-KKGCAMPPPCNPD 421

QY 417 TCRFKAGSNCAEGPCENCLFMSKERMCPSFECDLPYCNSSASCENPHVYVOTGHPC 476
DB 422 TKLSDSGSCSGICNSCKLKRGEVCRUAQDECDVTEYCNSTSEVC-EDDFVQNGHPC 480

QY 477 GLNQWICIDGVMGSKQKQCTDTFGKEVGFSPSEYCSYHLSKTDVSGNCGISDSGYTQCEA 536
DB 481 DNRKWCINGTCQSGEQCDLFGIDAGFSSSECFWELNSKSDISGSCGISAGYKECPP 540

QY 537 DNLQCKGLICKYGVKFLQIIPRATIIYANISGHLCIAVEFASDHADSKQWIKDGTSCGS 596
DB 541 NDRMCKGIIICKYQSENILKRSATVIYANISGHVCSLEYPOGHNESQKMWVRDGTVCGS 600

QY 597 NKVCRNORCVSSYLVGDCITTDKNDRGVNNKHKHCHCSASYLPPDCSVQSLWPQGSID 656
DB 601 NKVQONQKQVADTFLGVDNLEKNHGVNNKKNCHCDPTLPPDCRKNKDSYPGGSID 660

QY 657 SGNFPPVAIPARLPERRIENIYHSPMRPFLLFPFFIIFCVLIAMVKNVFORKKWR 716
DB 661 SGN-KERAEP--IPVRPIASRYRSKSPRPFLLIIPFFVIVLVLGMLVKVYSQRKKWR 717

QY 717 TEDIYSDDEQESSEPK 733
```

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Db 364 DFKFITSSSHCLQNPOTLPQSYK-MAVCGNGEVEDEICDGG-KKGCACEMPPPCNPD 421
Qy 417 TCRFKAGSNCAEGPCENCLFMSKERMCRPSFECDLPYCNCGSSASCENHYVQTHGPC 476
Db 422 TCKLSGSESCSGICCNCKLKRKEVRLAQDECDVTEYCNCTSEVC-BDFVQNGHPC 480
Qy 477 GLNQWICIDGVMSGDKQCTDTFGKEVEFGPSECYSHLNSKTVDVSGNCGISDSGTYQCEA 536
Db 481 DNRKWCINGTCQSGEQCQDLFGIDAGFGSSCFWELNSKSDISGSGISAGYKECPP 540
Qy 537 DNIQCKGLICKYVGKFLQIPRATIIYANISGHLCTIAVEFASDHADSOQMWIKDGTSCGS 596
Db 541 NDRMCGKIIKCYQSENILKLSATVIYANISGHVCSLEYFPQGHNESQKMWVRDGTVCGS 600
Qy 597 NKVCRNORCVSSSYLVGVDCTTDKNDRGVNNKKGCHCSASYLPDSCSVQSDLWPGSID 656
Db 601 NKVCQKQKQVADTFLGYDNCLEKHHGVNNKKNCHCDPTLYPPDCKRWKDSYFPGSID 660
Qy 657 SGNFPPVAIPARLPERRYENIYHSPKMRWPFLLIFPFFIIFCVLIAIMVKVNFQRKKWR 716
Db 661 SGN-KERAEP--IPVRPIASRYRSKSPRWPFFLLIFPVVILVLGMLVKVYSQRMKWR 717
Qy 717 TEDYSSDEQESSESEK 733
Db 718 MDDFSSBEQESSESEK 734

RESULT 8
US-08-264-101-4
; Sequence 4, Application US/08264101
; Patent No. 5693496
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAYWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,101
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-264-101-4

Query Match 38.0%; Score 1512; DB 1; Length 457;
Best Local Similarity 57.6%; Pred. No. 3.1e-116;
Matches 265; Conservative 74; Mismatches 115; Indels 6; Gaps 5;

Qy 274 SNYVGATFQKMCNDANYAGGVVLPRTISLESIAVLIAQLLSMGITVDDINKKCCSGA 333
Db 3 SDYVGATYQKMCNDKYNAGGVVLPRTISLESIAVLIAQLLSMGITVDDINKKCCGVP 62
Qy 334 VCIIMPPEALHFGSVKIFSNCSFEDFAHPTISKQSQCLHNPRLDPFFKQOAVCGNAKLEA 393
Db 63 VCVMPPEALHFGSVKIFSNCSMEDFSKFTSOSSHCLQNPOTLPQSYK-MAVCGNGEVE 121
Qy 394 GBECDGTBQDICALIGETCCDIATCRFKAGSNCAEGPCENCLFMSKERMCRPSFECDL 453
Db 122 DEICDGG-KKGCACEMPPPCNPDTCCKLSGSESCSGICCNCKLKRKEVRLAQDECDV 180
Qy 454 PEYCNCGSSASCENHYVQTHGPCGLNQWICIDGVMSGDKQCTDTFGKEVEFGPSECYSH 513
Db 181 TEYCNCTSEVC-EDFPVQNGHPCDNRKWCINGTCQSGEQCQDLFGIDAGFGSSECFWE 239
Qy 514 LNSKTDVSGNCGISDSGYTQCEADNLQCKLICKYVGKFLQIPRATIIYANISGHLCTIA 573
Db 240 LNSKSDISGSCGISAGYKECPPNDRMCGKIIKCYQSENILKLSATVIYANISGHVCS 299
Qy 574 VEFASDHADSOQMWIKDGTSCGSNKVCRNORCVSSSYLVGVDCTTDKNDRGVNNKKGCH 633
Db 300 LEYPOGHNESQKMWVRDGTVCGSNKVCQKQKQVADTFLGYDNCLEKHHGVNNKKNCH 359
Qy 634 CSASYLPDSCSVQSDLWPGSIDSGNFPFVAIPARLPERRYENIYHSPKMRWPFLLIFP 693
Db 360 CDPTLYPPDCKRWKDSYFPGSIDSGN-KERAEP--IPVRPIASRYRSKSPRWPFFLLIP 416
Qy 694 FFIIFCVLIAIMVKVNFQRKKWRTEDYSSDEQESSESEK 733
Db 417 FYVVLVLGMLVKVYSQRMKWRMDDFSSBEQESSESEK 456

RESULT 9
US-08-765-243-4
; Sequence 4, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAYWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-765-243-4

Query Match      38.0%; Score 1512; DB 2; Length 457;
Best Local Similarity 57.6%; Pred. No. 3.1e-116;
Matches 265; Conservative 74; Mismatches 115; Indels 6; Gaps 5;

Qy 274 SNVYGATFQGMCDANDYAGGVVLPRTISLESIAVLAQLLSMGITYDDINKCQCSGA 333
Db 3 SDVYGATYQGMCDKNYAGGVVLPRTISLESIAVLAQLLSMGITYDDINKCQCSGA 62
Qy 334 VCIWNPAAIHFSGVKIFSNCSFEDFAHFIKSKQSCCLHNPRLDPFFKQAVCGNAKLEA 393
Db 63 VCVNPEAPHSSGVRAFSNCSMEDFSKFIQSQSHCLQNPFTLPQSYK-MAVCGNGVEVE 121
Qy 394 GEECDCTEQDCCALIGETCCDIATCRFKAGSNCAEGPCCNCLFMSKERMCRPSFEBCDL 453
Db 122 DEICDCG-KKGCAMPPCCNPDTCKLSDGSECSGGICCNCKLKRKGEVCRLAQDECDV 180
Qy 454 PEYCNSSASCPENHYVQTHGPCGLNQMWCIDGVCMGDKQCTDTTPGKEVEFGPSECYSH 513
Db 181 TEYCNGTSEVC-EDFFVQNGHPCDNRKWCINGTCQSGEQCQDLFGIDAGFGSSECFWE 239
Qy 514 LNSKTDVSGNCGISDSGYTOCEADNLOGKLI CKYVGKFLLOIPRATIIIVANISGHLICIA 573
Db 240 LNSKSDISGSGISAGGYKECPNDRMCGKIICKYQSENILKRSATVIIVANISGHVCSV 299
Qy 574 VEFASDHADSQKMWIKDGTSGSNKVCNRCVSSSYLVGYDCTTDKCNDRGVCKNKKHCH 633
Db 300 LEVPOGHNESQKMWVRDGTVCNKKVCQNKQCVADTFGLVDCKLEKCNHHGVCKNKNCH 359
Qy 634 CSASYLPPDCSVQSDLWPGSIDSGNPPVAIPARLPERYIENIYHSKPMRPPFFLIP 693
Db 360 CDPTLYPPDCRKMDSYPGSIDSGN-KERAEP--IPVRPYIASRYSKSPRPFFLIIP 416
Qy 694 FFIIFCVLIAIMVKNFORKKWRTEDYSDEQSESESEPK 733
Db 417 FVYVILVLIGMLVKVYSQRMKRMDDFSSDEQSESESEK 456

RESULT 10
PCT-US95-07295-4
; Sequence 4, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07295-4

Query Match      38.0%; Score 1512; DB 5; Length 457;
Best Local Similarity 57.6%; Pred. No. 3.1e-116;
Matches 265; Conservative 74; Mismatches 115; Indels 6; Gaps 5;

Qy 274 SNVYGATFQGMCDANDYAGGVVLPRTISLESIAVLAQLLSMGITYDDINKCQCSGA 333
Db 3 SDVYGATYQGMCDKNYAGGVVLPRTISLESIAVLAQLLSMGITYDDINKCQCSGA 62
Qy 334 VCIWNPAAIHFSGVKIFSNCSFEDFAHFIKSKQSCCLHNPRLDPFFKQAVCGNAKLEA 393
Db 63 VCVNPEAPHSSGVRAFSNCSMEDFSKFIQSQSHCLQNPFTLPQSYK-MAVCGNGVEVE 121
Qy 394 GEECDCTEQDCCALIGETCCDIATCRFKAGSNCAEGPCCNCLFMSKERMCRPSFEBCDL 453
Db 122 DEICDCG-KKGCAMPPCCNPDTCKLSDGSECSGGICCNCKLKRKGEVCRLAQDECDV 180
Qy 454 PEYCNSSASCPENHYVQTHGPCGLNQMWCIDGVCMGDKQCTDTTPGKEVEFGPSECYSH 513
Db 181 TEYCNGTSEVC-EDFFVQNGHPCDNRKWCINGTCQSGEQCQDLFGIDAGFGSSECFWE 239
Qy 514 LNSKTDVSGNCGISDSGYTOCEADNLOGKLI CKYVGKFLLOIPRATIIIVANISGHLICIA 573
Db 240 LNSKSDISGSGISAGGYKECPNDRMCGKIICKYQSENILKRSATVIIVANISGHVCSV 299
Qy 574 VEFASDHADSQKMWIKDGTSGSNKVCNRCVSSSYLVGYDCTTDKCNDRGVCKNKKHCH 633
Db 300 LEVPOGHNESQKMWVRDGTVCNKKVCQNKQCVADTFGLVDCKLEKCNHHGVCKNKNCH 359
Qy 634 CSASYLPPDCSVQSDLWPGSIDSGNPPVAIPARLPERYIENIYHSKPMRPPFFLIP 693
Db 360 CDPTLYPPDCRKMDSYPGSIDSGN-KERAEP--IPVRPYIASRYSKSPRPFFLIIP 416
Qy 694 FFIIFCVLIAIMVKNFORKKWRTEDYSDEQSESESEPK 733
Db 417 FVYVILVLIGMLVKVYSQRMKRMDDFSSDEQSESESEK 456

RESULT 11
US-10-000-489-70
; Sequence 70, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 70
; LENGTH: 787
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..16
US-10-000-489-70

Query Match      37.8%; Score 1506.5; DB 4; Length 787;
Best Local Similarity 40.7%; Pred. No. 1.9e-115;
Matches 307; Conservative 135; Mismatches 261; Indels 51; Gaps 18;

QY 1 MWVFLSLGGLRMD-SNFDPLVQITVPEKIRSIIEKIEGIE---SQASQKIVIEGPKYT 56
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 LWL--LLAGCGLLASPGFQSLQLQIVPEKIQITNTDSSEIEYEIQISIIPIDEKLYT 61
QY 57 VNLQMKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGV 116
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VHLKQRYFLDNFWIYLYN-QGSNWTYSDDIQCYQGNIEEYFDSNMTLSICSLRGI 120
QY 117 LQFENVSYGIEPLESSVGFPHVIYQVHKKADVSLYNEKDIESR---DLSFKLQSAEPQ 173
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 LQFENVSYGIEPLESAVEFQVHLKLVNDNDIAIFIDRSLKEQPMDDNIFISEKSEFV 180
QY 174 D--FAKIEHVIYVERKOLYNHMGSDTTVAQKVPQLIGLITNAIFVSFNITIIISLELWI 231
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 PDLFPLYLEHIVVDKTLTYDYGSDSDMIVTNKVIIEIVGLANSMTQPKVTIVLSLELWS 240
QY 232 DENKIATGBANELLHTFLRWKTSYVLRPHDVAFLVYREKSNVYGATQGKMCADANYA 291
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 DENKISTVGADELLQKLEWKQSYLNLPHDIAIYLYWDYPRYLGAVPFGTWCITRYS 300
QY 292 GGVLVHPTISLESIAVILAQLLSMGITYDDINKCQCSGAVCIMNPEAHIFSGVKIFS 351
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 AGVALYKPEITLEAFVIVTQMLALSIGSYDDPKQCSESTCIMNPEVVSQNGVKTFS 360
QY 352 NCSFEDPAHISKQSOCLNQLRPDPFQKQAVCGNAKLEAGECDCTEQDCCALIGET 411
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 SCSLRSFQNFISNVGVKCLQNKPMQK-KGPKPYCGNGRLEGNEICDCGTEAQCG--PAS 417
QY 412 CCDIATCRKAGSNCAEGPCENCLFMSKERMCRP-SFEEDCLPEYCNCGSSASCENHYV 470
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
418 CDFRITCVLDGAKYKGLCKCKQCIILQSGVECPKAPHECDIAENCGNSPPEGPPITL 477
QY 471 QTGHPGCLNOMI CIDGVCMSGDQKCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGIS-DS 529
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
478 INGLSCKNNKFI CYDGDCHLDARCESVFGKSRNAPFACVEEIQSQSDRFGNCGDRNN 537
QY 530 GYTQCEADNLCQKLI CKYVKGKFLQIPRATIIYANISGHLCTIAVEPASDHADSQKWK 589
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
538 KYVFCGRNRLICGLRVCTYPRKPFHQENGDIYAFVRDSVCITVDYKLPRTVPDPLAVK 597
QY 590 DGTSCGSKNVCNRCORCVSSYL---GYDCTDKNDRGVNCKKHCHCSASYLPDPCSVQ 646
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
598 NGSQCDIGRCVNVRECVESRII KASAVC-SQQCSGHGVCDNRNKHCHSGYKPPNCQIR 656
QY 647 SLDWPGGSI---DSGNFPFVPAIPARLPERRYIENIYHSPMRW--PFFIIPFPIIFCV 700
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
657 S---KGFSIPEEDMGSI-----MERASGKTENTWLLGFLIALPILIV---696
QY 701 LIAIMVKNVQKWKRTEDYSSDRPQSESEPKG 734
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
697 -TTAIVLARKQLKNWFAKE---EEFPSSEKSEG 726

RESULT 12
US-10-140-002-116
; Sequence 116, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 116
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-116

Query Match      37.5%; Score 1493.5; DB 4; Length 715;
Best Local Similarity 40.3%; Pred. No. 1.9e-114;
Matches 302; Conservative 123; Mismatches 268; Indels 57; Gaps 14;

QY 3 VFLSLGGLRMDSNFDPLVQITVPEKIRSIIEKISQASQKIVIEGPKYTVMNQK 62
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 LLALLTELGRLOHEGSEGFILVTVPRKIKNSDSEVSEKMIYIITIDGQPYTLHLGKQ 63
QY 63 NPLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGPKSVVMVSTCTGLRGVLPENV 122
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
64 SFLPQNFVLTYNETSLSHSVSFYFMHCHYQYAAEFNPSFTLISCSLGRFLQFENI 123
QY 123 SYGIEPLESSVGFPHVIYQVHKKADVSL--YNEKDIESRDLSEFKLQSAEPQDFAK--- 177
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
124 SYGIEPESSARPEHIIYQKNNDPNVSLAVNYSYHIMQKQPKYKPLNSQIKNSKLLP 183
QY 178 -YTEMHVIVKQLYNHMGSDTTVAQKVPQLIGLITNAIFVSFNITIIISLELWIDENKI 236
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
184 QYLEIYIIVEKAL-----MFTQFKLTIVLSLELWSNENQI 219
QY 237 ATTGEANEILLHTFLRWKTSYVLRPHDVAFLVYREKSNVYGATFOGKMCADNAVAGVIL 296
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
220 STSGDADDILQRFIAWKRDYLLILRPHDIAIYLYVRKPKYVGTATFFGTCNKSVDAGIAM 279
QY 297 HPTISLESIAVILAQLLSMGITYDDINKCQCSGAVCIMNPEAHIFSGVKIFSNCSE 356
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
280 YPDAIGLEGFSEVIIAQLLGLNVLTVDDITQCFCLRATCINMHEAVSASGRKIFSNCSMH 339
QY 357 DPAHFTSKQSKQCLHNQPLDPFQKQAVCGNAKLEAGECDCTEQDCCALIGETCCDIA 416
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
340 DYRFYVSKFETKQLKSLNLQPLHQNPQVCGNGILESNEEDCGNKNQECOF--KKCCDYN 397
QY 417 TCRFKAGSNCAEGPCC-ENCLFMSKERMCRPSPE-ECDLPEYCNCGSSASCENHYVQTGH 474
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
398 TCKLKGSKVCGSGPCTSKCELSIAGTPCKRKSIDPECDFTTEYCNGTSSNCVPTYALNGR 457
QY 475 PCGLNOMI CIDGVCMSGDQKCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDQSGYTC 534
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
458 LCKLGTAYCNGQCTTNDQCAKIFGKGAQGAFFACFKEVNSLHSENGSGFKNSQPLPC 517
QY 535 EADNLCQKLI CKYVKGKFLQIPRATIIYANISGHLCTIAV----EFASDHADSQKWKID 590
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
518 ERKDVLCGLKACVQPHKNANKSDAQSTVYSYIDHVCVSTATGSSMRSDGTDN--AYVAD 575
QY 591 GTCGSKNVCNRCORCVSSYLGYDC-TTDCNDRGVNCKKHCHCSASYLPDPCSVQSDIL 649
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
576 GTWCGPEMYCNVTKRKVHLMGYNCAITKCKGKICNNFGNCQCPGHRPPDCKQFGS 635
```

Qy 650 WPGSIDSGNPPVAIPARLPERRIENIYHDKPMRW---PFLFPIPFPIFCVLIAMV 706
Db 636 -PGSIDDDGNF-----QKSGDFYTEKGYNTHWNWFIILSPCIFLFPFVFTVI---F 684
Qy 707 KVNFORKWRTE--DYSSDQSESESPKG 734
Db 685 KRNEISKCRNENAYNRNVSSESDDVG 714

RESULT 13
US-10-140-002-204
; Sequence 204, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 204
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-204

Query Match 23.8%; Score 948.5; DB 4; Length 790;
Best Local Similarity 32.0%; Pred. No. 1.8e-69;
Matches 254; Conservative 124; Mismatches 292; Indels 123; Gaps 30;
Qy 6 LLSGLGG---LRMDSNFDLSPVQITVPEKI--RSIIKEGIESQASYKIVIEGPKYTVNLM 60
Db 22 LLSGLGSDVIFHPEGEFDS--YEVTIPEKLSFRGEV-QGVVSPVSYLLQLKGGKHVLHW 78
Qy 61 QKN-FLPHNFRVSYSGTGIMKPLDQDFQNFCHYQVIEGPKSVVMVSTCT-GLRVQL 118
Db 79 PKRLLPRLHVRVSTFEGHELLEDHPYIPKDCNYMGSKVESLDSKATISTCMGRLRGVFN 138
Qy 119 FENVSYGIEPLESSVGFEHVIYQVKKKADVSLYNEKDIERSDLSFKLQSAEPQDF--- 175
Db 139 IDAKHYIEPLKASPFEHVHVIYLLKKEQFGNQVCGLSDDSEIEMQAPYENKARLURDPGS 198
Qy 176 ---AKYIEMHIVIEKQIYNHMGSDTTVVAQKVFOLIGLTNAIFVSNITILLSSLELWID 232
Db 199 YKHPKYLELILLPDQSYRFRVNNLSQVHDAILLTGIMDTYFQDVRMRHILKALEWTD 258
Qy 233 ENKIAT--TGANELLHTFLRWKTSYLVR-PhdVAFLLVYREKSNVYVATFGQKMCNANY 290
Db 259 FNKIRVGYPELAEVLGRFVIYKKSVLNARLSSWAHLQKRYNDALAWSF-GKVCSELEY 317
Qy 291 AGGV-----VLHPTISLESVALIQAQLLSMGITYDDINKCOCGAV-CTMNPFAI 342
Db 318 AGSVSTLLDNTILAPATWS-----AHELGHAVGMSHDE-QYCQCRGLNLCIMG---- 364
Qy 343 HFSGVKIFSCSPEDFAHFIISKQSKQLCHNQPRLDPPFKQAVCGNKALEAGEBCDCGTE 402

Db 365 --SGRTGFSNCSYISFFKHIS--SGATCLNNIPGLGYVLKR---CGNKIVEDNEEDCGST 418
Qy 403 QDCALLGETCCDIATCRFKAGSNCAEGPCCECNCLFMSKERMCMRSPSFECOLPEYCNSSA 462
Db 419 EECQ--KORCCQ--SNCKLOFGANCSIGLCCDCHDFRPSGYVCRQEGNECDLAEYCDGNSS 475
Qy 463 SCPENHYVQTHGPCGLNQWICIDGVCMSGDKQCTDTFTGKEVFEFSPSCYSHLSKTDVSG 522
Db 476 SCPNDVYKQDGTCKY-EGRCFRKCRSRVYMQQSIFGPDAMEAPSECYDAVNLIGDQFG 534
Qy 523 NCGISD--SGYTOCEADNLQCKLIKVKYVGFELQIPRATIIYANISHLCTIAVEFASDHA 581
Db 535 NCEITGIRNFKCESANSICRQLQCNV-ETIPDLPEHTTI---ISHL-----QA 581
Qy 582 DSQKMW-----IKDGTSCGNKVCNRQCRVSSSYLVGLDCTTKCNDR 623
Db 582 ENLMCWGTGYHLSMKPMGIPDLGMINDTSCGSGRVCFKNCVNSVLPQDFCLPEKCNTR 641
Qy 624 GVCNNKXCHCSASYLPDCSVQSDLWPGSIDSGNPPVPAIPARLPERRIENIYHSPK 683
Db 642 GVCNNRKNCHCMYGWAPPFC---EEVGYGGSIDSG--PPGLLRGAIPSSIWVSI----- 691
Qy 684 MRWPFPLPIPFPIFCVLIAMV-----KVNFORKKWRT-EDY 720
Db 692 -----IMFRLILLISLVVFFRQVIGNHLKPKOERKMLSKAKTEQESKTKTVQEE 743
Qy 721 SSDEQPESESEPK 733
Db 744 SKYTKQEESEAK 756

US-09-617-145-2
; Sequence 2, Application US/09617145
; Patent No. 6485956
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; TITLE OF INVENTION: SVPHI-8 DNA and Polypeptides
; FILE REFERENCE: 03260.0050-00304
; CURRENT APPLICATION NUMBER: US/09/617,145
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/071,505
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-617-145-2
Query Match 23.5%; Score 937; DB 4; Length 722;
Best Local Similarity 31.0%; Pred. No. 1.4e-68;
Matches 219; Conservative 133; Mismatches 284; Indels 70; Gaps 24;
Qy 1 MWVLLSLGGLGRMDSNFDLSPVQITVPEKIRSIIEGIESQA---SYKIVIEGPKYT 56
Db 17 LNLGVFLISIGYQAGPSQHTSPFVVIPDK---VISRGRSAKAPGWLSTLRFGGKHV 73
Qy 57 VNLQMKNFL-PhnFRVSYSGTGIMKPLDQDF-QNFCHYQVIEGPKSVVMVSTC-TGL 113
Db 74 VHMVRKLLVSRHLPVFTYTDERALLE-DQLFIPDDCYHYGVGEGAFESLVVFSACFGF 132
Qy 114 RGVLFENVSYGIEPLESSVGFEHVIYQVKKKADVSL-----YNEKDIERSDLSF---KL 166
Db 133 RGVLKISGLTYEIEIRHSATFELHVVYKNSNETQFPAMRCGLTEKEVARQQLFEFAEN 192
Qy 167 QSAEPQ-----DFAKYIEMHIVIEKQIYNHMGSDTTVVAQKVFOLIGLTNAIFVSNIT 221
Db 193 SALEPKSAGDWTHAWFLELVVNVHDFIYISQNSIKVQEDVFLVNVNIQQQLGTY 252
Qy 222 ILLSSLELWIDENKIATTTGANELLHTFLRWKTSYLVRPhdVAFLLVYREKSNVYVATF 281


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Db 253 IILIGBIWQGNVFPMT-SIEQVINDFSQWKQISLSQLQHDAAHMFKNLSLSILGLAY 311
Qy 282 QGKMCDA-----NYAGGVVHLPTTISLESVALAQLLSLSMGITYDDINKQCGSGAV 334
Db 312 VAGICRPPIDCGVDNFGD-----TWSL--FANTVAHELHTLGMQHDE-EFCFCGERG 362
Qy 335 CIMNPEAHFSGVKIFGSCFEDFAHFISSKQSCQLNQPRLDPPFFQQAQVCGNAKLEAG 394
Db 363 CIMNTPRV--PAEKFTNCYADPMKTTNLQGS-CLANPPRLGIFMLKR-CGNGVVERE 417
Qy 395 BECDGTEQCALIGETCCDIATCRFAGSNCAEGPCENCLFMSKERMCRPSFEBCDLP 454
Db 418 EQCDGSGVOQCE--QDACC-LLNCTLRPGAACAFGLCKCKDKFMPSELCRQEVNECDLP 474
Qy 455 EYCNNGSASCPENHYVOTGHPCLGNQWICIDGVCMSGDKOCTDFFGKEVFGPSECYSHL 514
Db 475 EWCNGTSHQCPEDRYVQDGIPCSQAY-CYQKRCNNHDDHCRREIFGDKASQNCYKEI 533
Qy 515 NSKTDVSGNGCISDSGYTQCEADNLOCGKLCYKVGKPLLIQIPRATIIYANISGHLCAV 574
Db 534 NSQNGRFGHCGINGTTYLKCHISDVFCGRVQCVENRDIPLLQDHFTLQHTHINGVTCWI 593
Qy 575 EF-----ASHADSQRWIIKDGTCGSKNKVCNRQRCVSSSYLGVDCTTDKCNDRGVGNK 629
Db 594 DYHLRMNISDGE-----VKDGTVCGPCKICHHKCVSLSVLHVCLPETCNMKGICNNK 648
Qy 630 KHCHCSASYLPDCSVQSDLWPGGSDSGN-----FPPVAIPA 667
Db 649 HHCHCGWNSPPYQHRG---YGGSDSGPASAKRGVFLPLIVIPS 691
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RESULT 15

```
US-09-786-256C-15
; Sequence 15, Application US/09786256C
; Patent No. 6680189
; GENERAL INFORMATION:
; APPLICANT: YOSHIMURA, Koji
; APPLICANT: HIKICHI, Yuichi
; APPLICANT: NISHIMURA, Atsushi
; TITLE OF INVENTION: No. 6680189el Protein and DNA Thereof
; FILE REFERENCE: 2544 USOP
; CURRENT APPLICATION NUMBER: US/09/786,256C
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/JP99/04766
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: JP 10-250115
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(775)
; OTHER INFORMATION: An isolated ADAM family protein
US-09-786-256C-15
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Query Match 21.2%, Score 843.5; DB 4; Length 775;
Best Local Similarity 28.9%, Pred. No. 8.1e-61;
Matches 210; Conservative 121; Mismatches 300; Indels 95; Gaps 23;

Qy 29 PEKIRSIIEGIESQASQYKIVIEGKPYTVNLMO-KNPLPHNFRVYSYSGTGMKPLDQDF 87
Db 47 PEQ-----QEQFETELKYKMTINGKIAVLKKNKLLAPGYTETYNSTGKEITTSFQI 101
Qy 88 QNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIBPLE--SSVGFPEHVI--YQVK 143
Db 102 MDDCYQGHILNEKVSQASISTCTGLRGYSQGRYFIPLSPIHRDQGEHALFKXNPD 161
Qy 144 HKKADVSLYNEKDIETSRDLS-----FKLQSAEPQDQAKYIEMHVIVEKQLYNHM 193
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Db 162 EKNYDSTCGMDGVLWADLQONIALPATKLVKLKDRK-VQEHEKYIEYIYLVLDNGEPKRY 220
Qy 194 GSOTTVVAQKVFOLIGLTNAIFVSFNITIISSLELWIDENKIATTCEANELLHTFLRWK 253
Db 221 NENQDEIRKRVFEMANYVMYKLLTHVALVGMETWTDKDKIKITPNASFTLENFSKWR 280
Qy 254 TSYLVLRP-HDVAFLVYRE-KSNYVGATFQGMKCDANYAGGVVLHPTTISLESVALA 311
Db 281 GSVLSRRKRHDIAQLTATATELAGTTVGLAFMTMC-SPYSVGVV-QDHSNLLRVAGTMA 338
Qy 312 QLLSLSGITYDDINKQCGSGAVCIWNPRAIHFSGVKIFSNCSFEDFAHFISSKQSCQLH 371
Db 339 HEMGHNFMPHDDYS-CKCPSTTCVMD-KALSFYIPTDFSSCSRLSYDKFFEDKLSNCLF 396
Qy 372 NQRLDPPFFQQAQVCGNAKLEAGEECDCGTQEOCALIGETCCDIATCRFAGSNCAEGPC 431
Db 397 NAP-LPTDIIISTPICNQLVEMGEDCCTGSECTWI---CCDAKTKIKATQCALGEC 452
Qy 432 CENCLFMSKERMCRPSFEBCDLPPEYCNNGSASCPENHYVOTGHPCLGNQWICIDGVCMG 491
Db 453 CEKQCFKAGMVCRAKDECDLPEMCMGKSGNCPDORFQVNGFPFCHHGKGLMGTCTPL 512
Qy 492 DKQCTDTFGKEVFGPSECYSHLSKTDVSGNGCISDSGYTQCEADNLOCGKLCIK--- 547
Db 513 QEQCTBLWGPTEVADKSCYNR-NEGSKYGYCRRVDDTLIPCKANDTMCGLKLPFCGGSD 571
Qy 548 ---YVGKFLLIQIPRATIIYANISGHLCAVEFASDHADSOKMWIKDGTSCGSKNKVCNRQ 604
Db 572 NLPWKGRIVTFLCKT-----FDPEDTSQEIGMVANGTKCDKNKVCINAE 616
Qy 605 CV---SSSYLGVDCTTDKCNDRGVGNKKGCHCSASYLPDCSVQSDLWPGGSDSGNFP 662
Db 617 CVDIEKAYKSTNCSS-KCXGHAVCDHELOQCQCEGWIPDPDCCDSS----- 660
Qy 663 VALPARLPERRYENIYHSPKPMWPFLLFPFPIIFCVLIAIMVKNVFNQKRWTEDEYSS 722
Db 661 -----VVFHFSIVVGVLV---PMAVIF-VVYAMVIRHQSSREKQK-----K 697
Qy 723 DEOPES 728
Db 698 DQRPLS 703
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Search completed: January 10, 2005, 22:29:19

Job time : 42 secs